

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 145 150 155

<210> 565

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(577)

<223> FRXA02249

<400> 565

atgttcgata cctgaaaacc aagcgtgacc gcatggggaca tgacctccca gatgtcgcac 60

tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115
 Met Ala Lys Glu Gly
 1 5

ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val
 10 15 20

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His
 25 30 35

gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259
 Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg
 40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307
 Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg
 55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355
 Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr
 70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403
 Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg
 90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451
 Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr
 105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499
 Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val
 120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547
 Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu

135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597
 Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 150 155

ttg 600

<210> 566
 <211> 159
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 566
 Met Ala Lys Glu Gly Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly
 1 5 10 15
 Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp
 20 25 30
 Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr
 35 40 45
 Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val
 50 55 60
 Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val
 65 70 75 80
 Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr
 85 90 95
 Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn
 100 105 110
 Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly
 115 120 125
 Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala
 130 135 140
 Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 145 150 155

<210> 567
 <211> 702
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(679)
 <223> RXA02250

<400> 567
 caactgaggg ttagactgtt ctttaaaagg tttgacgcct cggtttaatg cctagcagga 60
 tgcgcgccac cgctaattag ttctaaggat ttgtgaaatc gtg aca acc aac gcc 115
 Val Thr Thr Asn Ala

	1	5	
ccc gac gga gca acg aac aac atc aac aac gca cat tcg ggc gct gtc			163
Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala His Ser Gly Ala Val	10	20	
ggg aag cca aag gta cag ctc agc gat gcg gaa att cag gaa tac acc			211
Gly Lys Pro Lys Val Gln Leu Ser Asp Ala Glu Ile Gln Glu Tyr Thr	25	35	
gca gct ttc gct ggc acc acc aca acc aag cca tgg gag ctg gag gtg			259
Ala Ala Phe Ala Gly Thr Thr Thr Lys Pro Trp Glu Leu Glu Val	40	50	
acc aca aag ttt ctg aaa aag atc gcg tgg gta gcc gtg gtt gtc atc			307
Thr Thr Lys Phe Leu Lys Lys Ile Ala Trp Val Ala Val Val Val Ile	55	65	
atg gcc gtt cac atc ttc atg ggt gcc gtg gtg gac gtc gat ttc acc			355
Met Ala Val His Ile Phe Met Gly Ala Val Val Asp Val Asp Phe Thr	70	85	
ggt gca gcg gtc acc ttt gtt gac act ctg gca ttc cca gcg ttg ggc			403
Gly Ala Ala Val Thr Phe Val Asp Thr Leu Ala Phe Pro Ala Leu Gly	90	100	
atc atc ttc tcc gtt ctt gtg ttc ttg gga ctg act cgc cct cgc gtg			451
Ile Ile Phe Ser Val Leu Val Phe Leu Gly Leu Thr Arg Pro Arg Val	105	115	
cgt gcc aac gaa gac ggc gtt gag gtg cgt aac ttc atc gga act cgt			499
Arg Ala Asn Glu Asp Gly Val Glu Val Arg Asn Phe Ile Gly Thr Arg	120	130	
ttc tac cca tgg gtt gtc atc tac ggc atg tct ttc ccc aag ggc agc			547
Phe Tyr Pro Trp Val Val Ile Tyr Gly Met Ser Phe Pro Lys Gly Ser	135	145	
agc gtg gca cgt ttg gag ctt cca gac ttt gaa ttc gtt ccc atg tgg			595
Ser Val Ala Arg Leu Glu Leu Pro Asp Phe Glu Phe Val Pro Met Trp	150	165	
gct ttc cag tcc cgc gat gga gaa gat gtg gtg cgc gcg gtt gcg acc			643
Ala Phe Gln Ser Arg Asp Gly Glu Asp Val Val Arg Ala Val Ala Thr	170	180	
ttc cgc gac ctc gaa aac aag tac atg cca gag gac taattaagct			689
Phe Arg Asp Leu Glu Asn Lys Tyr Met Pro Glu Asp	185	190	
gtggctgac caa			702

<210> 568

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 568

Val	Thr	Thr	Asn	Ala	Pro	Asp	Gly	Ala	Thr	Asn	Asn	Ile	Asn	Asn	Ala
1				5				10							15

His	Ser	Gly	Ala	Val	Gly	Lys	Pro	Lys	Val	Gln	Leu	Ser	Asp	Ala	Glu
			20					25					30		
Ile	Gln	Glu	Tyr	Thr	Ala	Ala	Phe	Ala	Gly	Thr	Thr	Thr	Thr	Lys	Pro
		35					40					45			
Trp	Glu	Leu	Glu	Val	Thr	Thr	Lys	Phe	Leu	Lys	Lys	Ile	Ala	Trp	Val
	50					55					60				
Ala	Val	Val	Val	Ile	Met	Ala	Val	His	Ile	Phe	Met	Gly	Ala	Val	Val
65					70					75					80
Asp	Val	Asp	Phe	Thr	Gly	Ala	Ala	Val	Thr	Phe	Val	Asp	Thr	Leu	Ala
				85					90					95	
Phe	Pro	Ala	Leu	Gly	Ile	Ile	Phe	Ser	Val	Leu	Val	Phe	Leu	Gly	Leu
		100						105					110		
Thr	Arg	Pro	Arg	Val	Arg	Ala	Asn	Glu	Asp	Gly	Val	Glu	Val	Arg	Asn
		115					120					125			
Phe	Ile	Gly	Thr	Arg	Phe	Tyr	Pro	Trp	Val	Val	Ile	Tyr	Gly	Met	Ser
	130					135					140				
Phe	Pro	Lys	Gly	Ser	Ser	Val	Ala	Arg	Leu	Glu	Leu	Pro	Asp	Phe	Glu
145					150					155					160
Phe	Val	Pro	Met	Trp	Ala	Phe	Gln	Ser	Arg	Asp	Gly	Glu	Asp	Val	Val
				165					170					175	
Arg	Ala	Val	Ala	Thr	Phe	Arg	Asp	Leu	Glu	Asn	Lys	Tyr	Met	Pro	Glu
		180						185					190		

Asp

```
<210> 569
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1123)  
<223> RXA01489
```

<400> 569
gtcatgggat gtcattccgg cgggcttgtc gacgatcacg agtccaggtt taggggcagg 60

agcattcatg tctgttgagt ctatgccgta gtctaaaaca gtg gat att tgg agt 115
Val Asp Ile Trp Ser
1 5

gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att 163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile
10 15 20

ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag 211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu

25				30				35								
gcc	aag	aag	cag	gcc	gag	gag	ctg	ggt	gtg	cct	tgt	gtc	atg	gtg	acc	259
Ala	Lys	Lys	Gln	Ala	Glu	Glu	Leu	Gly	Val	Pro	Cys	Val	Met	Val	Thr	
		40					45					50				
ttt	gac	ccg	cat	ccg	atc	gct	gtg	ttt	ttg	cca	ggt	aaa	gag	cca	acc	307
Phe	Asp	Pro	His	Pro	Ile	Ala	Val	Phe	Leu	Pro	Gly	Lys	Glu	Pro	Thr	
	55				60						65					
cgt	ttg	gct	cct	ttg	gat	tat	cgc	ctt	aat	ttg	gct	gcg	gaa	tgt	ggc	355
Arg	Leu	Ala	Pro	Leu	Asp	Tyr	Arg	Leu	Asn	Leu	Ala	Ala	Glu	Cys	Gly	
	70				75				80						85	
gtc	gat	gct	gcg	ttg	gtt	att	gat	ttc	act	aaa	gaa	ctc	gca	ggg	ctg	403
Val	Asp	Ala	Ala	Leu	Val	Ile	Asp	Phe	Thr	Lys	Glu	Leu	Ala	Gly	Leu	
				90					95					100		
agc	gct	gaa	gag	tat	ttc	aca	acc	atg	atc	gtg	gat	acg	ctg	cat	gcg	451
Ser	Ala	Glu	Glu	Tyr	Phe	Thr	Thr	Met	Ile	Val	Asp	Thr	Leu	His	Ala	
			105					110					115			
cgt	tca	gtt	gtg	gtg	ggg	gag	aac	ttc	acc	ttc	ggt	gtc	aat	ggc	gct	499
Arg	Ser	Val	Val	Val	Gly	Glu	Asn	Phe	Thr	Phe	Gly	Val	Asn	Gly	Ala	
		120				125						130				
ggc	act	gag	tcc	acg	atg	cgg	gaa	ttg	gga	caa	aag	ttt	ggc	gtg	aat	547
Gly	Thr	Glu	Ser	Thr	Met	Arg	Glu	Leu	Gly	Gln	Lys	Phe	Gly	Val	Asn	
	135					140					145					
gtc	acg	att	gct	ccg	ctg	ctg	cat	gat	gat	gac	cag	cgt	att	tgc	tcc	595
Val	Thr	Ile	Ala	Pro	Leu	Leu	His	Asp	Asp	Asp	Gln	Arg	Ile	Cys	Ser	
	150				155					160					165	
acc	ttg	gtg	cgc	gat	tac	ttg	gat	cag	ggc	gag	gtt	gag	cgc	gcg	aac	643
Thr	Leu	Val	Arg	Asp	Tyr	Leu	Asp	Gln	Gly	Glu	Val	Glu	Arg	Ala	Asn	
				170				175						180		
tgg	gcg	ctt	ggt	cga	cgc	tat	gcc	gtg	cgc	ggc	gaa	gtt	gtc	cgt	ggg	691
Trp	Ala	Leu	Gly	Arg	Arg	Tyr	Ala	Val	Arg	Gly	Glu	Val	Val	Arg	Gly	
			185				190						195			
gct	ggc	cgt	ggc	ggc	aaa	gaa	ttg	ggc	tat	ccc	acc	gcg	aat	ctc	tac	739
Ala	Gly	Arg	Gly	Gly	Lys	Glu	Leu	Gly	Tyr	Pro	Thr	Ala	Asn	Leu	Tyr	
		200				205						210				
ctg	ccg	acc	tct	gtg	gcg	ctg	ccc	gcc	gat	ggc	gtg	tat	gca	ggc	tgg	787
Leu	Pro	Thr	Ser	Val	Ala	Leu	Pro	Ala	Asp	Gly	Val	Tyr	Ala	Gly	Trp	
		215				220					225					
ttc	acc	atc	acc	gat	gac	cgc	gaa	atc	gac	aag	gaa	atc	tcc	cgc	gat	835
Phe	Thr	Ile	Thr	Asp	Asp	Arg	Glu	Ile	Asp	Lys	Glu	Ile	Ser	Arg	Asp	
	230				235					240					245	
atc	gac	ggc	acc	atg	gtt	cca	ggc	gtg	cgt	tac	caa	act	gcc	att	tcc	883
Ile	Asp	Gly	Thr	Met	Val	Pro	Gly	Val	Arg	Tyr	Gln	Thr	Ala	Ile	Ser	
				250				255						260		
gtg	ggc	acc	aat	ccc	acc	ttc	ggc	gat	gag	cga	cgc	agc	gtc	gag	gca	931
Val	Gly	Thr	Asn	Pro	Thr	Phe	Gly	Asp	Glu	Arg	Arg	Ser	Val	Glu	Ala	
			265					270					275			

ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val
 280 285 290
 gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac
 1027
 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp
 295 300 305
 gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc
 1075
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile
 310 315 320 325
 ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct
 1123
 Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala
 330 335 340
 taaggccggt caccggccat caa
 1146

<210> 570
 <211> 341
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 570
 Val Asp Ile Trp Ser Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly
 1 5 10 15
 Ser Val Val Thr Ile Gly Val Phe Asp Gly Leu His Arg Gly His Gln
 20 25 30
 Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro
 35 40 45
 Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro
 50 55 60
 Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu
 65 70 75 80
 Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys
 85 90 95
 Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val
 100 105 110
 Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe
 115 120 125
 Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln
 130 135 140
 Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp
 145 150 155 160
 Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu

165										170					175				
Val	Glu	Arg	Ala	Asn	Trp	Ala	Leu	Gly	Arg	Arg	Tyr	Ala	Val	Arg	Gly				
			180					185					190						
Glu	Val	Val	Arg	Gly	Ala	Gly	Arg	Gly	Gly	Lys	Glu	Leu	Gly	Tyr	Pro				
		195					200					205							
Thr	Ala	Asn	Leu	Tyr	Leu	Pro	Thr	Ser	Val	Ala	Leu	Pro	Ala	Asp	Gly				
	210					215					220								
Val	Tyr	Ala	Gly	Trp	Phe	Thr	Ile	Thr	Asp	Asp	Arg	Glu	Ile	Asp	Lys				
225					230				235						240				
Glu	Ile	Ser	Arg	Asp	Ile	Asp	Gly	Thr	Met	Val	Pro	Gly	Val	Arg	Tyr				
				245				250						255					
Gln	Thr	Ala	Ile	Ser	Val	Gly	Thr	Asn	Pro	Thr	Phe	Gly	Asp	Glu	Arg				
			260					265					270						
Arg	Ser	Val	Glu	Ala	Phe	Ile	Leu	Asp	Gln	Glu	Ala	Asp	Leu	Tyr	Gly				
		275					280					285							
His	His	Val	Met	Val	Glu	Phe	Val	Gly	His	Leu	Arg	Asp	Met	Val	Lys				
	290					295					300								
Phe	Asn	Gly	Val	Asp	Glu	Leu	Leu	Asp	Ala	Met	Ala	Arg	Asp	Val	Thr				
305					310				315						320				
Asn	Ala	Arg	Asp	Ile	Leu	Ala	Lys	Asp	Lys	Leu	Leu	Leu	Asp	Ala	Asp				
				325					330					335					
Thr	Gln	Pro	Ser	Ala															
				340															

<210> 571

<211> 1197

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1174)

<223> RXA02135

<400> 571

cgtgtcgcag cgatttgcga gagggttgtc ttcgtgggtg ctggtctgcc actagagttg 60

aaaacgtttt	aagaaaacag	tcggtttgaa	ggagttgtta	atg gtt cca gca gag	115
				Met Val Pro Ala Glu	
				1 5	

ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg	163
Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr	
10 15 20	

aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag	211
Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys	
25 30 35	

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg	259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro	
40 45 50	
cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac	307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His	
55 60 65	
ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg	355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu	
70 75 80 85	
cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att	403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile	
90 95 100	
gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac	451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp	
105 110 115	
cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc	499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile	
120 125 130	
gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag	547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys	
135 140 145	
atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att	595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile	
150 155 160 165	
tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc	643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala	
170 175 180	
ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc	691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg	
185 190 195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc	739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile	
200 205 210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc	787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala	
215 220 225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc	835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe	
230 235 240 245	
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt	883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val	
250 255 260	
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc	931
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala	
265 270 275	
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc	979

Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser
 280 285 290
 gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg
 1027
 Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met
 295 300 305
 tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag
 1075
 Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys
 310 315 320 325
 att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc
 1123
 Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly
 330 335 340
 gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg
 1171
 Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr
 345 350 355
 gag taactttcta agcgatgtcc ggc
 1197
 Glu

<210> 572
 <211> 358
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 572
 Met Val Pro Ala Glu Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys
 1 5 10 15
 Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro
 20 25 30
 Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
 35 40 45
 Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
 50 55 60
 Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
 65 70 75 80
 Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
 85 90 95
 Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
 100 105 110
 Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
 115 120 125
 Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
 130 135 140

Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
 145 150 155 160
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
 165 170 175
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
 180 185 190
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
 195 200 205
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
 210 215 220
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
 225 230 235 240
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
 245 250 255
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
 260 265 270
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
 275 280 285
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
 290 295 300
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
 305 310 315 320
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
 325 330 335
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala
 340 345 350
 Pro Glu Gln Asn Thr Glu
 355

<210> 573
 <211> 1146
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1123)
 <223> RXA01489

<400> 573
 gtcattgggat gtcattccgg cgggcttgct gacgatcacg agtccagggt taggggcagg 60
 agcattcatg tctgttgagt ctatgccgta gtctaaaaca gtg gat att tgg agt 115
 Val Asp Ile Trp Ser
 1 5

gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att	163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile	
10 15 20	
ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag	211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu	
25 30 35	
gcc aag aag cag gcc gag gag ctg ggt gtg cct tgt gtc atg gtg acc	259
Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr	
40 45 50	
ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc	307
Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr	
55 60 65	
cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc	355
Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly	
70 75 80 85	
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg	403
Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu	
90 95 100	
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg	451
Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala	
105 110 115	
cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct	499
Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala	
120 125 130	
ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat	547
Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn	
135 140 145	
gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc	595
Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp Gln Arg Ile Cys Ser	
150 155 160 165	
acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac	643
Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn	
170 175 180	
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt	691
Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly	
185 190 195	
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac	739
Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr	
200 205 210	
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg	787
Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp	
215 220 225	
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat	835
Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp	
230 235 240 245	
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc	883

Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser
 250 255 260

gtg ggc acc aat ccc acc ttc ggc gat gag cga cgc agc gtc gag gca 931
 Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg Arg Ser Val Glu Ala
 265 270 275

ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val
 280 285 290

gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac
 1027
 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp
 295 300 305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc
 1075
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile
 310 315 320 325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct
 1123
 Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala
 330 335 340

taaggccggt caccggccat caa
 1146

<210> 574
 <211> 341
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 574
 Val Asp Ile Trp Ser Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly
 1 5 10 15

Ser Val Val Thr Ile Gly Val Phe Asp Gly Leu His Arg Gly His Gln
 20 25 30

Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro
 35 40 45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro
 50 55 60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu
 65 70 75 80

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys
 85 90 95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val
 100 105 110

Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe
 115 120 125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln

130 135 140
 Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp
 145 150 155 160
 Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu
 165 170 175
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly
 180 185 190
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro
 195 200 205
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly
 210 215 220
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys
 225 230 235 240
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr
 245 250 255
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg
 260 265 270
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly
 275 280 285
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys
 290 295 300
 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr
 305 310 315 320
 Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp
 325 330 335
 Thr Gln Pro Ser Ala
 340

<210> 575
 <211> 805
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (87)..(782)
 <223> RXN01712

<400> 575
 gccggccttag gctcctccga ccagaacccc actggcacct ttggataaca ccattccgtg 60
 taaacaagct ggcctagact tgaaacatg gtc gat atc ttg gaa ctc atc ggt 113
 Met Val Asp Ile Leu Glu Leu Ile Gly
 1 5
 ccc cta cct ttt gtg tct acg cca gag tta agg gca att gtc gtg act 161
 Pro Leu Pro Phe Val Ser Thr Pro Glu Leu Arg Ala Ile Val Val Thr

10	15	20	25	
gcc att aat ggt tcc acc act att aat ggc acg tct ggt cag ctt gga	209			
Ala Ile Asn Gly Ser Thr Thr Ile Asn Gly Thr Ser Gly Gln Leu Gly				
30 35 40				
aat tcc acg gat acg gaa ctt ctg ttg gcg ctt cgc agg tgg tcg gac	257			
Asn Ser Thr Asp Thr Glu Leu Leu Leu Ala Leu Arg Arg Trp Ser Asp				
45 50 55				
gtg gtg ttg gtt ggg tcg agc acg gtg aag gct gaa aat tat ggt ggc	305			
Val Val Leu Val Gly Ser Ser Thr Val Lys Ala Glu Asn Tyr Gly Gly				
60 65 70				
gtg gag gtt tcg cct gaa atc cag aag caa cgc cag gag ttg ggt cag	353			
Val Glu Val Ser Pro Glu Ile Gln Lys Gln Arg Gln Glu Leu Gly Gln				
75 80 85				
gaa gcg att ccg ccg att gcg gtg atg tca ggg tcg ttg aat ttt gat	401			
Glu Ala Ile Pro Pro Ile Ala Val Met Ser Gly Ser Leu Asn Phe Asp				
90 95 100 105				
gtg gat act cgc ttt ttc ctt gag gcc gaa gtg ccg ccg atc atc atc	449			
Val Asp Thr Arg Phe Phe Leu Glu Ala Glu Val Pro Pro Ile Ile Ile				
110 115 120				
acg gat aat tcc gat caa gca aag cag cag ccg ctt gtg gat gct ggg	497			
Thr Asp Asn Ser Asp Gln Ala Lys Gln Gln Arg Leu Val Asp Ala Gly				
125 130 135				
gct cag gtt att gag gtg gag acg ttg acg gcg gag gtt ggc gtc gaa	545			
Ala Gln Val Ile Glu Val Glu Thr Leu Thr Ala Glu Val Gly Val Glu				
140 145 150				
aag ctt agg tct ttg ggt tac gcc cgc att gat tgt gag ggc ggt gca	593			
Lys Leu Arg Ser Leu Gly Tyr Ala Arg Ile Asp Cys Glu Gly Gly Ala				
155 160 165				
acg ttg tat ggg cag atg ttg gcc gcc gat ctt gtt gat gtg tgg cat	641			
Thr Leu Tyr Gly Gln Met Leu Ala Ala Asp Leu Val Asp Val Trp His				
170 175 180 185				
cac acg att gat ccg acg ttg tcg ggc agc gtg gag cgc ccc acg gtg	689			
His Thr Ile Asp Pro Thr Leu Ser Gly Ser Val Glu Arg Pro Thr Val				
190 195 200				
aag ggc ggc gat gat gcg ccg cgc cga ttc gcg ttg gag cac gtc ttt	737			
Lys Gly Gly Asp Asp Ala Pro Arg Arg Phe Ala Leu Glu His Val Phe				
205 210 215				
gtc gat gat gac agc acc cta ttc ttg cgg tat aag cgc gcc aag	782			
Val Asp Asp Asp Ser Thr Leu Phe Leu Arg Tyr Lys Arg Ala Lys				
220 225 230				
tgagtgttgg actctccgga tct	805			

<210> 576

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 576

Met Val Asp Ile Leu Glu Leu Ile Gly Pro Leu Pro Phe Val Ser Thr
 1 5 10 15

Pro Glu Leu Arg Ala Ile Val Val Thr Ala Ile Asn Gly Ser Thr Thr
 20 25 30

Ile Asn Gly Thr Ser Gly Gln Leu Gly Asn Ser Thr Asp Thr Glu Leu
 35 40 45

Leu Leu Ala Leu Arg Arg Trp Ser Asp Val Val Leu Val Gly Ser Ser
 50 55 60

Thr Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile
 65 70 75 80

Gln Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala
 85 90 95

Val Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu
 100 105 110

Glu Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala
 115 120 125

Lys Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu
 130 135 140

Thr Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr
 145 150 155 160

Ala Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu
 165 170 175

Ala Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu
 180 185 190

Ser Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro
 195 200 205

Arg Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu
 210 215 220

Phe Leu Arg Tyr Lys Arg Ala Lys
 225 230

<210> 577

<211> 578

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (55) .. (555)

<223> FRXA01712

<400> 577

cttctgttgg cgcttcgcag gtgggtcggac gtgggtgttg ttgggtcgag cacggtg 57
 Val

1

```

aag gct gaa aat tat ggt ggc gtg gag gtt tcg cct gaa atc cag aag 105
Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln Lys
      5              10              15

caa cgc cag gag ttg ggt cag gaa gcg att ccg ccg att gcg gtg atg 153
Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val Met
      20              25              30

tca ggg tcg ttg aat ttt gat gtg gat act cgc ttt ttc ctt gag gcc 201
Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu Ala
      35              40              45

gaa gtg ccg ccg atc atc atc acg gat aat tcc gat caa gca aag cag 249
Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys Gln
      50              55              60              65

cag cgg ctt gtg gat gct ggg gct cag gtt att gag gtg gag acg ttg 297
Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr Leu
      70              75              80

acg gcg gag gtt ggc gtc gaa aag ctt agg tct ttg ggt tac gcc cgc 345
Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala Arg
      85              90              95

att gat tgt gag ggc ggt gca acg ttg tat ggg cag atg ttg gcc gcc 393
Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala Ala
      100              105              110

gat ctt gtt gat gtg tgg cat cac acg att gat ccg acg ttg tcg ggc 441
Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser Gly
      115              120              125

agc gtg gag cgc ccc acg gtg aag ggc ggc gat gat gcg ccg cgc cga 489
Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg Arg
      130              135              140              145

ttc gcg ttg gag cac gtc ttt gtc gat gat gac agc acc cta ttc ttg 537
Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe Leu
      150              155              160

cgg tat aag cgc gcc aag tgagtgttgg actctccgga tct 578
Arg Tyr Lys Arg Ala Lys
      165

```

<210> 578

<211> 167

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 578

```

Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln
  1              5              10              15

Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val
      20              25              30

Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu
      35              40              45

```

Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys
 50 55 60

Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr
 65 70 75 80

Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala
 85 90 95

Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala
 100 105 110

Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser
 115 120 125

Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg
 130 135 140

Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe
 145 150 155 160

Leu Arg Tyr Lys Arg Ala Lys
 165

<210> 579

<211> 831

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(808)

<223> RXN02384

<400> 579

ctgatgaggc ggatatccgc aacatcgaca gcattgatga actcccacct ttgccagctg 60

aatacgagcc tggctacgag gacgattaag aggtagtcct gtg act cgt cgc ctg 115
 Val Thr Arg Arg Leu
 1 5

att ctg ctc cga cac ggg cag act gaa tac aac gcc acg tcc cga atg 163
 Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn Ala Thr Ser Arg Met
 10 15 20

cag gga caa ttg gac aca gag ctg tct gac ctg ggc ttt caa cag gcg 211
 Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu Gly Phe Gln Gln Ala
 25 30 35

gcc agc gca gcc tca gtg ctg gtt caa aaa aac atc acc cat gtg ttc 259
 Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn Ile Thr His Val Phe
 40 45 50

agc tcg gat ctt tcc cgc gcc ttc aac acc gca agc gcg gtt gcg gcg 307
 Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala Ser Ala Val Ala Ala
 55 60 65

ctg att gac gcg gag gtg cgc gtc gat aag cgt ctt cgg gaa acg cat 355
 Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg Leu Arg Glu Thr His

70	75	80	85	
ttg ggt gag tgg cag gcc aaa acc cac act gag gtg gat tcc gaa tat				403
Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu Val Asp Ser Glu Tyr				
	90	95	100	
cca ggt gcg cgc gct caa tgg cgc cac gat ccg cag tgg gca cca ccc				451
Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro Gln Trp Ala Pro Pro				
	105	110	115	
ggc ggc gaa tcg cgc gtg gat gtt gcg cgc cgg gca cgc caa gtt gtc				499
Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg Ala Arg Gln Val Val				
	120	125	130	
gac gag ttg atg gtg tcg ctt gat gat tgg gat gaa ggc acc gtg ctc				547
Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp Glu Gly Thr Val Leu				
	135	140	145	
atc gtg gct cac ggt ggc acg att aat gcg ctg acc tcg aat ctt ttg				595
Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu Thr Ser Asn Leu Leu				
	150	155	160	165
gac ctg gcg tat gat cag tac ccc atg ttc tct gga ctt gga aat acc				643
Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser Gly Leu Gly Asn Thr				
	170	175	180	
tgt tgg gca caa ttg acc gcc cga cct cgc tat tat gca ggt agt gag				691
Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr Tyr Ala Gly Ser Glu				
	185	190	195	
aac cca gaa gat gac ctc aag att tct tcg gcg gtt tcc aac agc cct				739
Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala Val Ser Asn Ser Pro				
	200	205	210	
cat ttt gag ggc aac aat gtg gaa aac gcc cag tgg tat ctt gac ggc				787
His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln Trp Tyr Leu Asp Gly				
	215	220	225	
tgg aac atg ggt gtt acg cag taaagaagat ggcaataaaa atg				831
Trp Asn Met Gly Val Thr Gln				
	230	235		

<210> 580

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 580

Val Thr Arg Arg Leu Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn				
1	5	10	15	
Ala Thr Ser Arg Met Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu				
	20	25	30	
Gly Phe Gln Gln Ala Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn				
	35	40	45	
Ile Thr His Val Phe Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala				
	50	55	60	

Ser Ala Val Ala Ala Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg
 65 70 75 80
 Leu Arg Glu Thr His Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu
 85 90 95
 Val Asp Ser Glu Tyr Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro
 100 105 110
 Gln Trp Ala Pro Pro Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg
 115 120 125
 Ala Arg Gln Val Val Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp
 130 135 140
 Glu Gly Thr Val Leu Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu
 145 150 155 160
 Thr Ser Asn Leu Leu Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser
 165 170 175
 Gly Leu Gly Asn Thr Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr
 180 185 190
 Tyr Ala Gly Ser Glu Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala
 195 200 205
 Val Ser Asn Ser Pro His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln
 210 215 220
 Trp Tyr Leu Asp Gly Trp Asn Met Gly Val Thr Gln
 225 230 235

<210> 581

<211> 453

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(430)

<223> RXN01560

<400> 581

atgggagcaa ggctcattta gctacttcga cgtggaagcg cacatcggtg agttgattcc 60
 tgcacagta agcgatgcgt tttaggcaca tctgcgatcc gtg ggc gtg tcc tac 115
 Val Gly Val Ser Tyr
 1 5
 atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa 163
 Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys
 10 15 20
 att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga 211
 Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly
 25 30 35
 acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc 259
 Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser

40	45	50	
atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg			307
Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu			
55	60	65	
ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca			355
Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser			
70	75	80	85
ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac			403
Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr			
90	95	100	
ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc			450
Gly Val Asn Gly Pro Val Asp Ala Asn			
105	110		
ttt			453

<210> 582

<211> 110

<212> PRT

<213> Corynebacterium glutamicum

<400> 582

Val Gly Val Ser Tyr Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala
1 5 10 15

Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile
20 25 30

Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu
35 40 45

Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys
50 55 60

His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu
65 70 75 80

Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser
85 90 95

Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn
100 105 110

<210> 583

<211> 1137

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1114)

<223> RXN00667

<400> 583

ggcatcagtg tttgaaggga aaagcaggtc aaacaaggtg cggtctgattt gagcgatcac 60

agcaccgaga tctgtgctga agaattcaat gattgggttg atg att gcg ttg aag	115
Met Ile Ala Leu Lys	
1 5	
tcc atg tct aac agg gta gta caa aag cca aaa atg aaa gcg ccg cta	163
Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys Met Lys Ala Pro Leu	
10 15 20	
ccc atc cgc gac ggc ctc aac cct tcc cgt gtg cgc ttg ccg ctc gac	211
Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val Arg Leu Pro Leu Asp	
25 30 35	
gcg gcg ccg atc cgc gcc atc gat ttt gtt gaa tac ctc att tcc acg	259
Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu Tyr Leu Ile Ser Thr	
40 45 50	
cag cgc cac cgc aat ccg gcc gac aac gcc gaa gcg ctt caa gcg cgt	307
Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu Ala Leu Gln Ala Arg	
55 60 65	
ttc gac gcc gac ctt gtt gtc aac cac tac ggc gag ccc tac gcc ccc	355
Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly Glu Pro Tyr Ala Pro	
70 75 80 85	
gac acc atg gtt cag ccc gac gac gac att tgg ttc tac cgc atg ccc	403
Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp Phe Tyr Arg Met Pro	
90 95 100	
gcc gcc gaa cgg ccg atc cct tac aaa att cat gtc att cac gaa gac	451
Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His Val Ile His Glu Asp	
105 110 115	
gat gac atc ctc gtc att gac aag cca ccc tac cta gca acc atg cct	499
Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr Leu Ala Thr Met Pro	
120 125 130	
cgt ggc cgc cac atc acc gaa acc gct ctg gtg aaa atg cgt gtg ctg	547
Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val Lys Met Arg Val Leu	
135 140 145	
act gga aac aac gat ctc acc cca gct cac cgc ctc gat cgc ctg act	595
Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg Leu Asp Arg Leu Thr	
150 155 160 165	
tcc ggt gtg tta gtc atg gtg aaa aaa cca gaa ctc cgt ggc gct tac	643
Ser Gly Val Leu Val Met Val Lys Lys Pro Glu Leu Arg Gly Ala Tyr	
170 175 180	
caa acc ttg ttt gcc cga cgt gag gcg tcc aaa acc tat gag gca atc	691
Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys Thr Tyr Glu Ala Ile	
185 190 195	
gca gaa ttc gtt cca ggg cta ctt gat gat ggt ccc gcg att tgg gaa	739
Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly Pro Ala Ile Trp Glu	
200 205 210	
tcc cgc atc gaa aaa gaa cgc ggc atc gtg caa gcc ttc gtc gtg gaa	787
Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln Ala Phe Val Val Glu	
215 220 225	

ggc ccc gtc aac gca cgc act gaa ctg gtg tca gtc acc cca gtc gaa 835
 Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser Val Thr Pro Val Glu
 230 235 240 245

gac gcc gaa cag agc atc ctc gaa gaa atg cac ggg cca ctc ccc cgc 883
 Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His Gly Pro Leu Pro Arg
 250 255 260

caa gcg cgc tac gtt cta gcc ccc tca aca ggc aaa acc cac cag ctg 931
 Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly Lys Thr His Gln Leu
 265 270 275

cgc atc cac atg cgc gac ttc gca gcc ccc atc ctc ggc gac ccc ctc 979
 Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile Leu Gly Asp Pro Leu
 280 285 290

tac ccc gtc ctc cac gca gtc gac gat gag gac tac acc acc cca atg
 1027
 Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp Tyr Thr Thr Pro Met
 295 300 305

cac ctc atc gcc cgc acg cta acc ttc gtg gat cct caa acc aac gag
 1075
 His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp Pro Gln Thr Asn Glu
 310 315 320 325

gaa cgt acc ttt gtg agt aat cga cct acg gga agt ttg taggcctcgt
 1124
 Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly Ser Leu
 330 335

agacatcacc cag
 1137

<210> 584

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 584

Met Ile Ala Leu Lys Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys
 1 5 10 15

Met Lys Ala Pro Leu Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val
 20 25 30

Arg Leu Pro Leu Asp Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu
 35 40 45

Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu
 50 55 60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly
 65 70 75 80

Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp
 85 90 95

Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His
 100 105 110

Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr
 115 120 125
 Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val
 130 135 140
 Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg
 145 150 155 160
 Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu
 165 170 175
 Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys
 180 185 190
 Thr Tyr Glu Ala Ile Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly
 195 200 205
 Pro Ala Ile Trp Glu Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln
 210 215 220
 Ala Phe Val Val Glu Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser
 225 230 235 240
 Val Thr Pro Val Glu Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His
 245 250 255
 Gly Pro Leu Pro Arg Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly
 260 265 270
 Lys Thr His Gln Leu Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile
 275 280 285
 Leu Gly Asp Pro Leu Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp
 290 295 300
 Tyr Thr Thr Pro Met His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp
 305 310 315 320
 Pro Gln Thr Asn Glu Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly
 325 330 335

Ser Leu

<210> 585

<211> 1281

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1258)

<223> RXC01711

<400> 585

tctcgtgagt ttctccccg tagcaccttc tatatcagcc cccacgccgc gtcggagcag 60

gtgggatagc atcggcaacg cggttgcatg gccgttgccc atg ttg ttg atg gcg 115

											Met 1	Leu	Leu	Met	Ala 5	
cat His	cgc Arg	ttc Phe	ttc Phe	gtg Val 10	ctt Leu	gcg Ala	att Ile	aac Asn	ggc Gly 15	gca Ala	gtc Val	acc Thr	gac Asp	gat Asp 20	ttc Phe	163
acg Thr	acg Thr	gtt Val	tat Tyr 25	agt Ser	gct Ala	tta Leu	cga Arg	cgt Arg 30	ttc Phe	gtt Val	gaa Glu	ggg Gly	att Ile 35	ccg Pro	gtc Val	211
tac Tyr	aac Asn	gag Glu 40	gtc Val	tac Tyr	cac His	ttc Phe	gtc Val 45	gat Asp	ccg Pro	cac His	tac Tyr	ctc Leu 50	tat Tyr	aac Asn	ccg Pro	259
ggc Gly	gcc Ala 55	acc Thr	ctc Leu	cta Leu	ttg Leu	gca Ala 60	cca Pro	ttg Leu	gga Gly	tat Tyr	atc Ile 65	acc Thr	cat His	ttc Phe	acg Thr	307
ttg Leu 70	gct Ala	cgg Arg	tgg Trp	atg Met	ttc Phe 75	atc Ile	gcg Ala	gtg Val	aac Asn	ctc Leu 80	ctt Leu	gcc Ala	att Ile	gtt Val	tta Leu 85	355
gcg Ala	ttc Phe	ggg Gly	ctg Leu	ctg Leu 90	acc Thr	aga Arg	ctc Leu	tcc Ser	ggg Gly 95	tgg Trp	gcg Ala	ctg Leu	cgc Arg	agc Ser 100	atg Met	403
gtg Val	tgg Trp	ccg Pro	att Ile 105	gcg Ala	atc Ile	gcc Ala	ttg Leu 110	gcg Ala	atg Met	ctg Leu	aca Thr	gaa Glu	acc Thr 115	gtg Val	caa Gln	451
aac Asn	acc Thr	ctc Leu 120	att Ile	ttc Phe	tcc Ser	aac Asn	atc Ile 125	aac Asn	ggc Gly	atc Ile	ctg Leu 130	ctg Leu	ctc Leu	atg Met	ttg Leu	499
gcg Ala	att Ile 135	ttc Phe	ctg Leu	tgg Trp	tgc Cys	gtg Val 140	gtg Val	cac His	aaa Lys	aaa Lys	tcc Ser 145	tgg Trp	ttg Leu	ggc Gly	gga Gly	547
cta Leu 150	gtc Val	att Ile	ggg Gly	ttg Leu	gcc Ala 155	att Ile	ttg Leu	atc Ile	aaa Lys	ccc Pro 160	atg Met	ttc Phe	ctg Leu	cca Pro	ctt Leu 165	595
ctc Leu	ttc Phe	cta Leu	cct Pro	ttg Leu 170	gtg Val	aaa Lys	aag Lys	caa Gln	tgg Trp 175	gga Gly	tcg Ser	ctc Leu	atc Ile	ctc Leu 180	ggc Gly	643
att Ile	tta Leu	acc Thr	cca Pro 185	gtg Val	att Ile	ttc Phe	aat Asn	gca Ala 190	gtg Val	gcc Ala	tgg Trp	ttc Phe	tta Leu 195	gtt Val	ccg Pro	691
gga Gly	gca Ala	tct Ser 200	gaa Glu	tac Tyr	gtc Val	acc Thr	cgc Arg	acg Thr	atg Met	ccc Pro	tac Tyr	ctt Leu 210	ggg Gly	gaa Glu	act Thr	739
cga Arg	gat Asp 215	ttt Phe	gcc Ala	aac Asn	agc Ser	tca Ser 220	ctc Leu	cca Pro	ggc Gly	ttg Leu	gcc Ala 225	atc Ile	tat Tyr	ttc Phe	gga Gly	787
atg Met	ccc Pro	acc Thr	tgg Trp	atg Met	gaa Glu	atc Ile	acc Thr	tgg Trp	ttc Phe	ctc Leu	atc Ile	ttc Phe	ggc Gly	gca Ala	atg Met	835

230 235 240 245
 gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca 883
 Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro
 250 255 260
 tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc 931
 Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe
 265 270 275
 ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct 979
 Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro
 280 285 290
 atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt
 1027
 Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val
 295 300 305
 gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc
 1075
 Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser
 310 315 320 325
 cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc
 1123
 Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr
 330 335 340
 gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc
 1171
 Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile
 345 350 355
 tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att
 1219
 Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile
 360 365 370
 acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt
 1268
 Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala
 375 380 385
 caaactcatc agc
 1281

<210> 586

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 586

Met Leu Leu Met Ala His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala
 1 5 10 15

Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val
 20 25 30

Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His

35	40	45
Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr		
50	55	60
Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu		
65	70	75
80		
Leu Ala Ile Val Leu Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp		
85	90	95
Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu		
100	105	110
Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile		
115	120	125
Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys		
130	135	140
Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro		
145	150	155
160		
Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly		
165	170	175
Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala		
180	185	190
Trp Phe Leu Val Pro Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro		
195	200	205
Tyr Leu Gly Glu Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu		
210	215	220
Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu		
225	230	235
240		
Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe		
245	250	255
Arg Asn Thr Glu Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu		
260	265	270
Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser		
275	280	285
Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val		
290	295	300
Phe His Asn Trp Val Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro		
305	310	315
320		
Asp Thr Phe Thr Ser Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu		
325	330	335
Phe Phe Ser Ala Thr Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe		
340	345	350
Val Ser Ala Leu Ile Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr		
355	360	365

Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg
 370 375 380

Thr Ala
 385

<210> 587

<211> 777

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(754)

<223> RXC02380

<400> 587

gcagattttt gacgaagtcg catcgtggat tgaagctgcc taaaaactcg cgaggacgca 60

tgctcagcaa ggtggtgtgc gaacactata ctgtccactc atg act aca acg gtg 115
 Met Thr Thr Thr Val
 1 5

aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163
 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile
 10 15 20

cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211
 His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp
 25 30 35

ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259
 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala
 40 45 50

aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307
 Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile
 55 60 65

gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat 355
 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp
 70 75 80 85

cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403
 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys
 90 95 100

caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451
 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu
 105 110 115

gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc 499
 Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala
 120 125 130

cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547
 His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile
 135 140 145

att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595
 ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala
 150 155 160 165

atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc 643
 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
 170 175 180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
 185 190 195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys
 200 205 210

ggc caa aac caa gca taaatctagt caaaagtttc aac 777
 Gly Gln Asn Gln Ala
 215

<210> 588

<211> 218

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 588

Met Thr Thr Thr Val Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly
 1 5 10 15

Thr Phe Asp Pro Ile His Asn Gly His Leu Val Ala Gly Ser Glu Val
 20 25 30

Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln
 35 40 45

Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr
 50 55 60

Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser
 65 70 75 80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu
 85 90 95

Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
 100 105 110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
 115 120 125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
 130 135 140

Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
 145 150 155 160

Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
 165 170 175

Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val

	180		185		190	
Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys						
195		200		205		
Asp Met Asp Pro Lys Gly Gln Asn Gln Ala						
210		215				
<210> 589						
<211> 777						
<212> DNA						
<213> Corynebacterium glutamicum						
<220>						
<221> CDS						
<222> (101)..(754)						
<223> FRXA02380						
<400> 589						
gcagattttt gacgaagtcg catcgtggat tgaagctgcc taaaaactcg cgaggacgca 60						
tgctcagcaa ggtggtgtgc gaacactata ctgtccactc		atg act aca acg gtg	115			
		Met Thr Thr Thr Val				
		1 5				
aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att			163			
Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile						
	10	15		20		
cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat			211			
His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp						
	25	30		35		
ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg			259			
Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala						
	40	45		50		
aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc			307			
Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile						
	55	60		65		
gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat			355			
Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp						
	70	75		80		85
cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag			403			
Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys						
	90	95		100		
caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg			451			
Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu						
	105	110		115		
gca cag atc gtg acg tgg gcg gat tgg gag aaa acc ttc gaa ctt gcc			499			
Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala						
	120	125		130		
cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc			547			
His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile						
	135	140		145		

```

att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595
Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala
150          155          160          165

atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc 643
Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
          170          175          180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691
Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
          185          190          195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739
Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys
          200          205          210

ggc caa aac caa gca taaatctagt caaaagtttc aac 777
Gly Gln Asn Gln Ala
215

```

<210> 590
 <211> 218
 <212> PRT
 <213> *Corynebacterium glutamicum*

```

<400> 590
Met Thr Thr Thr Val Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly
 1          5          10          15

Thr Phe Asp Pro Ile His Asn Gly His Leu Val Ala Gly Ser Glu Val
          20          25          30

Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln
          35          40          45

Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr
          50          55          60

Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser
          65          70          75          80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu
          85          90          95

Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
          100          105          110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
          115          120          125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
          130          135          140

Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
          145          150          155          160

Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
          165          170          175

```

Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val
180 185 190

Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys
195 200 205

Asp Met Asp Pro Lys Gly Gln Asn Gln Ala
210 215

<210> 591

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(571)

<223> RXC02921

<400> 591

tggaaaactg ggaagggttg acgttgcgga atctctccgc agcgtcgggtt cggaccctaa 60

aaaagggtga ggaaccacat gagctgtttt aaggaatttt gtg tct gca ctt gaa 115
Val Ser Ala Leu Glu
1 5

gag tcg atc cgc atc gcg acc atc gcg gcg aaa gca gcg gat gaa aag 163
Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys
10 15 20

aag gcc gat gac atc gct gtc atc gat gtc tct gac atg atc gca atc 211
Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile
25 30 35

acc gat tgc ttt gtt gtt gca tct gct gac aat gag cgc cag gtg ggc 259
Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn Glu Arg Gln Val Gly
40 45 50

gcc att gtt gag gag atc gaa gat gag atg acc aag gct ggt ttc gag 307
Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr Lys Ala Gly Phe Glu
55 60 65

cct aag cgc cgt gaa ggc aac cgc gaa aac cgt tgg gtt ctc ctt gac 355
Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp
70 75 80 85

tac gga ttg gtt gtt atc cac gtt cag cga cag gca gag cgc gag ttc 403
Tyr Gly Leu Val Val Ile His Val Gln Arg Gln Ala Glu Arg Glu Phe
90 95 100

tac gga ctg gat cgt ctg tac cgc gac tgc cca ctc att gaa att gaa 451
Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro Leu Ile Glu Ile Glu
105 110 115

gga ctt gaa acc ttc aag cgt gaa tcc tcc tgg tct gat gag gcg gat 499
Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp Ser Asp Glu Ala Asp
120 125 130

atc cgc aac atc gac agc att gat gaa ctc cca cct ttg cca gct gaa 547
Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro Pro Leu Pro Ala Glu

135 140 145 594
 tac gag cct ggc tac gag gac gat taagaggtag tcctgtgact cgt
 Tyr Glu Pro Gly Tyr Glu Asp Asp
 150 155

<210> 592
 <211> 157
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 592
 Val Ser Ala Leu Glu Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys
 1 5 10 15
 Ala Ala Asp Glu Lys Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser
 20 25 30
 Asp Met Ile Ala Ile Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn
 35 40 45
 Glu Arg Gln Val Gly Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr
 50 55 60
 Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg
 65 70 75 80
 Trp Val Leu Leu Asp Tyr Gly Leu Val Val Ile His Val Gln Arg Gln
 85 90 95
 Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro
 100 105 110
 Leu Ile Glu Ile Glu Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp
 115 120 125
 Ser Asp Glu Ala Asp Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro
 130 135 140
 Pro Leu Pro Ala Glu Tyr Glu Pro Gly Tyr Glu Asp Asp
 145 150 155

<210> 593
 <211> 3075
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(3052)
 <223> RXC01434

<400> 593
 gggttcctgc gcaccgtgat gattgggtgcg gcgctgtcgc cggccatcgc ttcggcggttc 60
 aacactgcc aacacgctgcc caacctgatc actggaaatc gtg ttg ggt gcg gtg 115
 Val Leu Gly Ala Val
 1 5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac	163
Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp	
10 15 20	
gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg	211
Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val	
25 30 35	
acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg	259
Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu	
40 45 50	
ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg	307
Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met	
55 60 65	
tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc	355
Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly	
70 75 80 85	
ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa	403
Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys	
90 95 100	
ccc gcc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg	451
Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val	
105 110 115	
ctg gcc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag	499
Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln	
120 125 130	
gtg gcc att ttt gat ccg cag atc att ttc ctc ggc gtg gcc acc acc	547
Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr	
135 140 145	
ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc	595
Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg	
150 155 160 165	
gcg gcc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag	643
Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys	
170 175 180	
caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc	691
Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	
185 190 195	
cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat	739
Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	
200 205 210	
gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct	787
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
215 220 225	
tat gcc atc atc gcc gtc acc ttg ctc acc gcg att atg ccg cga ctg	835
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
230 235 240 245	
tcc cgc aac gcg gca gac gcc gat gat agg gca gta gtc tct gac ctt	883

Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu
 250 255 260
 cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg 931
 Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val
 265 270 275
 ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac 979
 Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr
 280 285 290
 ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc
 1027
 Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser
 295 300 305
 ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg
 1075
 Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu
 310 315 320 325
 cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc
 1123
 Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile
 330 335 340
 gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg
 1171
 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu
 345 350 355
 ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac
 1219
 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn
 360 365 370
 ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc
 1267
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg
 375 380 385
 aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg
 1315
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu
 390 395 400 405
 tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg
 1363
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu
 410 415 420
 ggg tgg ctg att caa gcc gtc gtg ggc gat ttc ttg ctg ggc act cta
 1411
 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu
 425 430 435
 agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc
 1459
 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe
 440 445 450

atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc
1507

Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val
455 460 465

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt
1555

Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe
470 475 480 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag
1603

Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu
490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc
1651

Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr
505 510 515

cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg
1699

Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu
520 525 530

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat
1747

Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp
535 540 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc
1795

His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala
550 555 560 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc
1843

Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala
570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag
1891

Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu
585 590 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta
1939

Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val
600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg
1987

Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val
615 620 625

gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt
2035

Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly
630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc
2083

Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr
650 655 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag
2131

Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys
665 670 675

tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg
2179

Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc
2227

Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala
695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc
2275

Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val
710 715 720 725

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc
2323

Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro
730 735 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc
2371

Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr
745 750 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct
2419

Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro
760 765 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg
2467

Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met
775 780 785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc
2515

Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala
790 795 800 805

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa
2563

Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln
810 815 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct
2611

Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro
825 830 835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat
2659

Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp
840 845 850

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc
2707

Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser
855 860 865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc
2755

Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser
870 875 880 885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc
2803

Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser
890 895 900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc
2851

Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala
905 910 915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat
2899

Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr
920 925 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg
2947

Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro
935 940 945

ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca
2995

Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser
950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt
3043

Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu
970 975 980

gtt ggt tgg taaattacgc gtttgtgatt gac
3075

Val Gly Trp

<210> 594

<211> 984

<212> PRT

<213> Corynebacterium glutamicum

<400> 594

Val Leu Gly Ala Val Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg
1 5 10 15

Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu

20					25					30					
Leu	Thr	Leu	Ser	Val	Thr	Leu	Leu	Gly	Gly	Val	Thr	Ile	Leu	Ser	Ile
		35					40					45			
Ile	Gly	Ala	Pro	Leu	Leu	Thr	Arg	Met	Met	Leu	Ser	Ser	Glu	Gly	Gln
	50					55					60				
Val	Asn	Val	Val	Met	Ser	Thr	Ala	Phe	Ala	Tyr	Trp	Leu	Leu	Pro	Gln
65						70					75				80
Ile	Phe	Phe	Tyr	Gly	Leu	Phe	Ala	Leu	Phe	Met	Ala	Val	Leu	Asn	Thr
				85					90					95	
Arg	Glu	Val	Phe	Lys	Pro	Gly	Ala	Trp	Ala	Pro	Val	Val	Asn	Asn	Val
			100					105					110		
Ile	Thr	Leu	Thr	Val	Leu	Gly	Val	Tyr	Met	Val	Leu	Pro	Ala	Arg	Leu
	115					120					125				
His	Pro	His	Glu	Gln	Val	Gly	Ile	Phe	Asp	Pro	Gln	Ile	Ile	Phe	Leu
	130					135					140				
Gly	Val	Gly	Thr	Thr	Leu	Gly	Val	Val	Ala	Gln	Cys	Leu	Ile	Met	Ile
145						150					155				160
Pro	Tyr	Leu	Arg	Arg	Ala	Gly	Ile	Asp	Met	Arg	Pro	Leu	Trp	Gly	Ile
				165					170					175	
Asp	Ala	Arg	Leu	Lys	Gln	Phe	Gly	Gly	Met	Ala	Met	Ala	Ile	Ile	Val
			180					185					190		
Tyr	Val	Ala	Ile	Ser	Gln	Phe	Gly	Tyr	Ile	Ile	Thr	Thr	Arg	Ile	Ala
	195						200					205			
Ser	Ile	Ala	Asp	Asp	Ala	Ala	Pro	Phe	Ile	Tyr	Gln	Gln	His	Trp	Met
	210					215					220				
Leu	Leu	Gln	Val	Pro	Tyr	Gly	Ile	Ile	Gly	Val	Thr	Leu	Leu	Thr	Ala
225						230					235				240
Ile	Met	Pro	Arg	Leu	Ser	Arg	Asn	Ala	Ala	Asp	Gly	Asp	Asp	Arg	Ala
				245					250					255	
Val	Val	Ser	Asp	Leu	Gln	Leu	Gly	Ser	Lys	Leu	Thr	Phe	Ile	Ala	Leu
			260					265					270		
Ile	Pro	Ile	Val	Val	Phe	Phe	Thr	Ala	Phe	Gly	Val	Pro	Ile	Ala	Asn
	275						280					285			
Gly	Leu	Phe	Ala	Tyr	Gly	Gln	Phe	Asp	Ala	Asn	Ala	Ala	Asn	Ile	Leu
	290					295					300				
Gly	Trp	Thr	Leu	Ser	Phe	Ser	Ala	Phe	Thr	Leu	Ile	Pro	Tyr	Ala	Leu
305						310					315				320
Val	Leu	Leu	His	Leu	Arg	Val	Phe	Tyr	Ala	Arg	Glu	Glu	Val	Trp	Thr
				325					330					335	
Pro	Thr	Phe	Ile	Ile	Ala	Gly	Ile	Thr	Ala	Thr	Lys	Val	Val	Leu	Ser
			340					345					350		

Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu
 355 360 365
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly
 370 375 380
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
 385 390 395 400
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
 405 410 415
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
 420 425 430
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
 435 440 445
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
 450 455 460
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
 465 470 475 480
 Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val
 485 490 495
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser
 500 505 510
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val
 515 520 525
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe
 530 535 540
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln
 545 550 555 560
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
 565 570 575
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala
 580 585 590
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
 595 600 605
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
 610 615 620
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
 625 630 635 640
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
 645 650 655
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
 660 665 670

Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
 675 680 685
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
 690 695 700
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
 705 710 715 720
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
 725 730 735
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
 740 745 750
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
 755 760 765
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
 770 775 780
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val
 785 790 795 800
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser
 805 810 815
 Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser
 820 825 830
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln
 835 840 845
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr
 850 855 860
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu
 865 870 875 880
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr
 885 890 895
 Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr
 900 905 910
 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile
 915 920 925
 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp
 930 935 940
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp
 945 950 955 960
 Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile
 965 970 975
 Ala Glu Val Gln Leu Val Gly Trp
 980

<210> 595
 <211> 915
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(892)
 <223> RXA01807

<400> 595

```

gctcaccgag ctggacacca agctccgcgc agtgcaggaa gaacacggcg agctggaaat 60

gcagtggctg gaactcggcg aggaaatcga gggctagttc atg ccg tcg gca ggc 115
                                   Met Pro Ser Ala Gly
                                   1 5

gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163
Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg
                                   10 15 20

gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg 211
Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly
                                   25 30 35

ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259
Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val
                                   40 45 50

gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307
Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser
                                   55 60 65

cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac 355
His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp
                                   70 75 80 85

ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc 403
Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly
                                   90 95 100

tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag 451
Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln
                                   105 110 115

aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc 499
Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile
                                   120 125 130

atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc 547
Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr
                                   135 140 145

gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat 595
Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn
                                   150 155 160 165

gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg 643
Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu
                                   170 175 180

```

ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act 691
 Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr
 185 190 195
 gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa 739
 Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu
 200 205 210
 atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc 787
 Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val
 215 220 225
 tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc 835
 Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile
 230 235 240 245
 gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc 883
 Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr
 250 255 260
 aaa gcg ctt taggtttcgt ccgtctctga cag 915
 Lys Ala Leu

<210> 596

<211> 264

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 596

Met Pro Ser Ala Gly Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu
 1 5 10 15
 Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val
 20 25 30
 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
 35 40 45
 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
 50 55 60
 Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
 65 70 75 80
 Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser
 85 90 95
 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val
 100 105 110
 Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile
 115 120 125
 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala
 130 135 140
 Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr
 145 150 155 160

Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly
 165 170 175
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr
 180 185 190
 Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg
 195 200 205
 Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys
 210 215 220
 Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys
 225 230 235 240
 Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys
 245 250 255
 Ala Gly Leu Gln Thr Lys Ala Leu
 260

<210> 597
 <211> 1461
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1438)
 <223> RXN02754

<400> 597
 attatgaagc catcggagtt ggtgtggcct acaaggggtga tcatgcgtgg atagtgggtgg 60
 agttcactgt agctcccgct gattccgtag aatcaacaga gtg aat acc aat ccg 115
 Val Asn Thr Asn Pro
 1 5
 tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
 10 15 20
 gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211
 Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
 25 30 35
 ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259
 Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg
 40 45 50
 tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307
 Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp
 55 60 65
 ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355
 Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp
 70 75 80 85
 cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403
 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp

90										95					100					
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act	451																			
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr																				
105 110 115																				
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg	499																			
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu																				
120 125 130																				
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	547																			
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met																				
135 140 145																				
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	595																			
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg																				
150 155 160 165																				
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643																			
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala																				
170 175 180																				
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	691																			
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile																				
185 190 195																				
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	739																			
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn																				
200 205 210																				
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787																			
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu																				
215 220 225																				
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc	835																			
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr																				
230 235 240 245																				
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc	883																			
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly																				
250 255 260																				
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc	931																			
Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg																				
265 270 275																				
aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc	979																			
Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser																				
280 285 290																				
tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt																				
1027																				
Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val																				
295 300 305																				
gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca																				
1075																				
Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro																				
310 315 320 325																				

acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg
1123

Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val
330 335 340

gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct
1171

Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala
345 350 355

gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac
1219

Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr
360 365 370

cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc
1267

Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser
375 380 385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct
1315

Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro
390 395 400 405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta
1363

Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu
410 415 420

cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act
1411

Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr
425 430 435

cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca
1458

Arg Phe Val Gly Phe Pro Pro Ala Ala
440 445

aac
1461

<210> 598

<211> 446

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 598

Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu
1 5 10 15

Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp
20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
 65 70 75 80
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
 85 90 95
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
 115 120 125
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
 145 150 155 160
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
 165 170 175
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
 210 215 220
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
 225 230 235 240
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
 245 250 255
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu
 260 265 270
 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr
 275 280 285
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu
 290 295 300
 Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr
 305 310 315 320
 Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val
 325 330 335
 Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly
 340 345 350
 Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile
 355 360 365
 Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys
 370 375 380

Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile
385 390 395 400

Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys
405 410 415

Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu
420 425 430

Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala
435 440 445

<210> 599

<211> 871

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(871)

<223> FRXA02405

<400> 599

attatgaagc catcggagtt ggtgtggcct acaaggggtga tcatgcgtgg atagtgggtgg 60

agttcactgt agtctccgct gattccgtag aatcaacaga gtg aat acc aat ccg 115
Val Asn Thr Asn Pro
1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
10 15 20

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211
Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
25 30 35

ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg
40 45 50

tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp
55 60 65

ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp
70 75 80 85

cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp
90 95 100

ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act 451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr
105 110 115

gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg 499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu
120 125 130

tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg 547
 Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met
 135 140 145
 gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc 595
 Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg
 150 155 160 165
 acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct 643
 Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala
 170 175 180
 gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att 691
 Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile
 185 190 195
 cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac 739
 Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn
 200 205 210
 gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa 787
 Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu
 215 220 225
 tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc 835
 Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr
 230 235 240 245
 caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca 871
 Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro
 250 255

<210> 600

<211> 257

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 600

Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu
 1 5 10 15
 Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp
 20 25 30
 Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
 35 40 45
 Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
 50 55 60
 Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
 65 70 75 80
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
 85 90 95
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110

Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
 115 120 125

Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140

Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
 145 150 155 160

Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
 165 170 175

Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190

Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205

Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
 210 215 220

Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
 225 230 235 240

Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
 245 250 255

Pro

<210> 601
 <211> 509
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(486)
 <223> FRXA02754

<400> 601
 ccc aca aac acc aag att gtg gtc tcc tcc gac ctg gat gaa ttc gcc 48
 Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala
 1 5 10 15

atc gcg ggt ctt cgc ggc gaa cca gtt gac gtc ttt ggc gtt ggc acc 96
 Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
 20 25 30

tcc gtt gtc aca ggt tct ggc gca cca acc gct ggc ctc gtg tac aag 144
 Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
 35 40 45

atc ggg gaa gtt gcc ggt cac cct gtg gcc aag cgt tcc cga aac aag 192
 Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
 50 55 60

gaa agc tac ggt ggt ggc aag aag gct gtg cgc acc cac cgc aag tcc 240
 Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
 65 70 75 80

ggt acc gca atc gaa gaa atc gtc tac cca ttc aat gcc gaa gca cca 288
 Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
 85 90 95

gat act gga aag ctc gac act ttg agc ctg acc atc cca ttg atg cgc 336
 Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
 100 105 110

gac ggt gaa atc gtt cca ggt ttg cct act ttg gaa gat tcc cga gcg 384
 Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
 115 120 125

tat ttg gcc aag caa ttg gtc tct tta cca tgg gaa ggc ctt gca ctg 432
 Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
 130 135 140

tct cgc gat gag cct gtt ttg cac act cgt ttc gtg ggt ttc ccg ccg 480
 Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
 145 150 155 160

gcc gct tagacaattc ggtctcacca aac 509
 Ala Ala

<210> 602

<211> 162

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 602

Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala
 1 5 10 15

Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
 20 25 30

Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
 35 40 45

Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
 50 55 60

Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
 65 70 75 80

Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
 85 90 95

Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
 100 105 110

Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
 115 120 125

Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
 130 135 140

Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
 145 150 155 160

Ala Ala

<210> 603

<211> 960

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(937)

<223> RXA02112

<400> 603

```

tgaatccgtg gcggcaccgg cgcgagtcgc tttggaaagg atgctatctg ttgttccagc 60
agctcctgtt actcctagct cctcgaagga tgcgtaattt atg act acc cat att 115
                                         Met Thr Thr His Ile
                                         1                               5

gac cgc atc gtt ggc gca gcg tta tcc gag gat gcg cca tgg ggc gac 163
Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp Ala Pro Trp Gly Asp
                        10                        15                        20

att acc tcc gac act ttt atc cca gga tcg gcg cag ctg agc gcc aag 211
Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala Gln Leu Ser Ala Lys
                        25                        30                        35

gtt gtt gcc cgg gag cca ggt gtg ttc agc ggg cag gcg ctt tta gac 259
Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly Gln Ala Leu Leu Asp
                        40                        45                        50

gcc tcc ttc cgg ctc gtc gat cct agg ata aac gca tcc ctt aag gtg 307
Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn Ala Ser Leu Lys Val
                        55                        60                        65

gct gat ggt gac agc ttt gaa acc ggg gac atc cta gga aca att acc 355
Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile Leu Gly Thr Ile Thr
                        70                        75                        80                        85

ggc agt gct aga agc atc ctc cgt tca gag cgc att gct ctc aac ttc 403
Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg Ile Ala Leu Asn Phe
                        90                        95                        100

att cag agg acg tcc ggc atc gct aca ttg aca tcg tgc tat gtt gca 451
Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr Ser Cys Tyr Val Ala
                        105                        110                        115

gag gtt aaa ggc acc aaa gcc cgc att gtt gat acc cgg aaa acc aca 499
Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp Thr Arg Lys Thr Thr
                        120                        125                        130

ccc ggc ctg cgc atc att gaa cgc caa gct gtc cgt gac ggt ggc gga 547
Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val Arg Asp Gly Gly Gly
                        135                        140                        145

ttt aat cac cga gcc acc ttg tcc gat gct gtc atg gtg aaa gat aac 595
Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val Met Val Lys Asp Asn
150                        155                        160                        165

```

cat ctc gca gcc atc gca tcc cag ggg ctc agc atc act gaa gcg ctg 643
 His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser Ile Thr Glu Ala Leu
 170 175 180

tcg aat atg aaa gct aaa ctc ccc cac acc acc cat gtg gaa gtc gaa 691
 Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr His Val Glu Val Glu
 185 190 195

gtt gat cat ata gag cag atc gaa cca gtt ctt gct gct ggt gtg gac 739
 Val Asp His Ile Glu Gln Ile Glu Pro Val Leu Ala Ala Gly Val Asp
 200 205 210

acc atc atg ttg gat aat ttc acc att gat cag ctc atc gaa ggc gtt 787
 Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln Leu Ile Glu Gly Val
 215 220 225

gat ctc att ggt gga cgt gca ctg gtg gaa gca tct ggc gga gtc aac 835
 Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala Ser Gly Gly Val Asn
 230 235 240 245

ctc aac acc gcg gga aag att gca tca acc ggt gtc gac gtc att tcc 883
 Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly Val Asp Val Ile Ser
 250 255 260

gtt gga gcg ctt acc cat tct gtg cat gca ctt gac cta gga ctc gat 931
 Val Gly Ala Leu Thr His Ser Val His Ala Leu Asp Leu Gly Leu Asp
 265 270 275

att ttc taatgctcta ccttgataat gca 960
 Ile Phe

<210> 604

<211> 279

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 604

Met Thr Thr His Ile Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp
 1 5 10 15

Ala Pro Trp Gly Asp Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala
 20 25 30

Gln Leu Ser Ala Lys Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly
 35 40 45

Gln Ala Leu Leu Asp Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn
 50 55 60

Ala Ser Leu Lys Val Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile
 65 70 75 80

Leu Gly Thr Ile Thr Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg
 85 90 95

Ile Ala Leu Asn Phe Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr
 100 105 110

S r Cys Tyr Val Ala Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp
 115 120 125
 Thr Arg Lys Thr Thr Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val
 130 135 140
 Arg Asp Gly Gly Gly Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val
 145 150 155 160
 Met Val Lys Asp Asn His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser
 165 170 175
 Ile Thr Glu Ala Leu Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr
 180 185 190
 His Val Glu Val Glu Val Asp His Ile Glu Gln Ile Glu Pro Val Leu
 195 200 205
 Ala Ala Gly Val Asp Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln
 210 215 220
 Leu Ile Glu Gly Val Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala
 225 230 235 240
 Ser Gly Gly Val Asn Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly
 245 250 255
 Val Asp Val Ile Ser Val Gly Ala Leu Thr His Ser Val His Ala Leu
 260 265 270
 Asp Leu Gly Leu Asp Ile Phe
 275

<210> 605
 <211> 1407
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1384)
 <223> RXA02111

<400> 605
 gcttgcggga acaccgcacc gccaccccaa actgttcaga ttccaaagat aaattctgac 60
 gctcattcca gccaccggtt tagaagaaaa gaccccaatc atg acc acc tca atc 115
 Met Thr Thr Ser Ile
 1 5
 acc cca tct gtc aac ctt gca ttg aaa aat gcc aat agc tgc aac agt 163
 Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser
 10 15 20
 gaa ctc aaa gac gga ccc tgg ttc ctc gac cag ccc gga atg ccg gat 211
 Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln Pro Gly Met Pro Asp
 25 30 35
 gtc tac ggc ccc ggc gcg tca caa aac gat ccg atc cct gcg cat gct 259
 Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro Ile Pro Ala His Ala

40	45	50	
ccg cgc cag cag gtt ctc ccc gag gag tac cag cgc gca agt gat gac Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln Arg Ala Ser Asp Asp 55 60 65			307
gaa ctg cat cgt agg atc cgg gaa gcg aaa gac acc ctg ggt gac aaa Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp Thr Leu Gly Asp Lys 70 75 80 85			355
gtg gtt atc cta gga cac ttc tac cag cgc gat gaa gtt atc caa cac Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp Glu Val Ile Gln His 90 95 100			403
gca gat ttt gtt ggt gac tct ttc caa ctt gcc cgc gct gcc aaa acc Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala Arg Ala Ala Lys Thr 105 110 115			451
cga ccc gag gcg gaa gcg att gtg ttc tgc ggt gtg cac ttc atg gct Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly Val His Phe Met Ala 120 125 130			499
gaa acc gct gat ctg tta tcc acg gat gaa caa tca gtg atc ctc ccc Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln Ser Val Ile Leu Pro 135 140 145			547
aac ctt gcc gca ggt tgc tcc atg gca gac atg gct gac ctt gat tcc Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met Ala Asp Leu Asp Ser 150 155 160 165			595
gtc gaa gac tgc tgg gag caa ctc acc tca att tat ggc gat gac acc Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile Tyr Gly Asp Asp Thr 170 175 180			643
ctg atc cct gtg acc tac atg aat tcc tct gca gcg ctc aaa ggt ttc Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala Ala Leu Lys Gly Phe 185 190 195			691
gtg ggt gag cac ggc gga att gta tgc acc tcc tca aat gca cgt tcc Val Gly Glu His Gly Gly Ile Val Cys Thr Ser Ser Asn Ala Arg Ser 200 205 210			739
gta ttg gag tgg gcg ttt gaa cgc ggc caa cga gtc ctg ttc ttc ccc Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg Val Leu Phe Phe Pro 215 220 225			787
gat cag cac ttg ggt cga aac acc gcg aaa gcc atg ggc att ggg atc Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala Met Gly Ile Gly Ile 230 235 240 245			835
gat caa atg ccc ctg tgg aat ccc aac aaa cca ctg ggt ggc aac acc Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro Leu Gly Gly Asn Thr 250 255 260			883
gtt tcc gag cta gaa aac gca aag gta ctg ctc tgg cat ggt ttc tgc Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu Trp His Gly Phe Cys 265 270 275			931
tct gta cac aag cgc ttt act gtc gag cag atc aac aaa gcc cgc gcc Ser Val His Lys Arg Phe Thr Val Glu Gln Ile Asn Lys Ala Arg Ala 280 285 290			979

gag tac ccc gac gtt cac gtc atc gtg cac cct gaa tcc ccc atg cca
1027

Glu Tyr Pro Asp Val His Val Ile Val His Pro Glu Ser Pro Met Pro
295 300 305

gtt gtt gac gcc gcc gac tca tcc gga tcc act gac ttc att gtg aaa
1075

Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr Asp Phe Ile Val Lys
310 315 320 325

gcc att caa gca gca ccg gca gga tct acc ttt gcg atc ggc acc gaa
1123

Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe Ala Ile Gly Thr Glu
330 335 340

atc aac ttg gtt cag cgc ctg gca gcc cag tac ccg cag cac acc atc
1171

Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile
345 350 355

ttc tgc ctc gac cct gtc atc tgc cca tgc tcc acc atg tat cgc att
1219

Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile
360 365 370

cac cct ggt tac ctg gcc tgg gca ctt gag gag ttg gtg gct gga aac
1267

His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn
375 380 385

gtg att aac cag att tct gtc tct gaa tcc gtg gcg gca ccg gcg cga
1315

Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val Ala Ala Pro Ala Arg
390 395 400 405

gtc gct ttg gaa agg atg cta tct gtt gtt cca gca gct cct gtt act
1363

Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr
410 415 420

cct agc tcc tcg aag gat gcg taatttatga ctacccatat tga
1407

Pro Ser Ser Ser Lys Asp Ala
425

<210> 606

<211> 428

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 606

Met Thr Thr Ser Ile Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala
1 5 10 15

Asn Ser Cys Asn Ser Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln
20 25 30

Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro
35 40 45

Ile Pro Ala His Ala Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln
 50 55 60
 Arg Ala Ser Asp Asp Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp
 65 70 75 80
 Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp
 85 90 95
 Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala
 100 105 110
 Arg Ala Ala Lys Thr Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly
 115 120 125
 Val His Phe Met Ala Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln
 130 135 140
 Ser Val Ile Leu Pro Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met
 145 150 155 160
 Ala Asp Leu Asp Ser Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile
 165 170 175
 Tyr Gly Asp Asp Thr Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala
 180 185 190
 Ala Leu Lys Gly Phe Val Gly Glu His Gly Gly Ile Val Cys Thr Ser
 195 200 205
 Ser Asn Ala Arg Ser Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg
 210 215 220
 Val Leu Phe Phe Pro Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala
 225 230 235 240
 Met Gly Ile Gly Ile Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro
 245 250 255
 Leu Gly Gly Asn Thr Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu
 260 265 270
 Trp His Gly Phe Cys Ser Val His Lys Arg Phe Thr Val Glu Gln Ile
 275 280 285
 Asn Lys Ala Arg Ala Glu Tyr Pro Asp Val His Val Ile Val His Pro
 290 295 300
 Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr
 305 310 315 320
 Asp Phe Ile Val Lys Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe
 325 330 335
 Ala Ile Gly Thr Glu Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr
 340 345 350
 Pro Gln His Thr Ile Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser
 355 360 365

Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu
 370 375 380

Leu Val Ala Gly Asn Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val
 385 390 395 400

Ala Ala Pro Ala Arg Val Ala Leu Glu Arg Met Leu Ser Val Val Pro
 405 410 415

Ala Ala Pro Val Thr Pro Ser Ser Ser Lys Asp Ala
 420 425

<210> 607

<211> 954

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(931)

<223> RXA01073

<400> 607

taaccgactc cagcactaaa ctccaaaccc ttggcccgca ccgccaaagt ttagcgcgcc 60

ccaagacacc accgcgccat gtttgccctag gattaggtac atg aca aac act caa 115
 Met Thr Asn Thr Gln
 1 5

acc gag atc att aat gaa cta aag gtg agc cca gca atc gac gtg gcc 163
 Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro Ala Ile Asp Val Ala
 10 15 20

aag gaa gtt gaa ttc cgt gtg cag ttc ctc gtc gat tac ctg cgg gct 211
 Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val Asp Tyr Leu Arg Ala
 25 30 35

tcc cat aca aaa ggc ttt gtt ctt ggt att tca ggt ggc cag gat tcc 259
 Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser Gly Gly Gln Asp Ser
 40 45 50

act ctt gcg gga cga ctc acg cag ctg gca gta gag cgc att cgt gcg 307
 Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val Glu Arg Ile Arg Ala
 55 60 65

gaa gaa aac agc acg gat tat gtc ttc tac gca gtt cgc ctc ccc tac 355
 Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala Val Arg Leu Pro Tyr
 70 75 80 85

gcg atc cag gca gat gag gac gat gcg caa gtt gca ttg gaa ttc atc 403
 Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val Ala Leu Glu Phe Ile
 90 95 100

gca cct gac aag agc gtg acc gtc aac gtt aaa gac gca acg gac gcc 451
 Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys Asp Ala Thr Asp Ala
 105 110 115

acc gaa gca act gtt gca gct gct ttg gaa ctt cct gag ctg acc gac 499
 Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu Pro Glu Leu Thr Asp
 120 125 130

ttc aat cgg ggc aat att aaa gct cgc caa cgc atg gtt gcc cag tac 547
 Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg Met Val Ala Gln Tyr
 135 140 145

 gca atc gca ggc cag ttg ggc ttg ctg gtt att ggc act gat cac gcg 595
 Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile Gly Thr Asp His Ala
 150 155 160 165

 gct gaa aac gtc acg ggg ttc ttc acc aaa ttc ggt gat ggc gca gct 643
 Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly Ala Ala
 170 175 180

 gac ctg ctt cct ttg gca ggt ttg agc aag cgt caa gga gct gcc att 691
 Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg Gln Gly Ala Ala Ile
 185 190 195

 ctg gag cac ctg ggt gca cct tca agc acg tgg acc aag gtt cct acc 739
 Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp Thr Lys Val Pro Thr
 200 205 210

 gct gat ttg gaa gag gat cgc cca gcg ttg cca gat gag gaa gca ctt 787
 Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro Asp Glu Glu Ala Leu
 215 220 225

 ggt gtg tcg tat gcg gac atc gat aat tac ctg gaa aac aag ccc gat 835
 Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu Glu Asn Lys Pro Asp
 230 235 240 245

 gtc agt gaa aaa gcc cag cag cgc att gag cac ctg tgg aag gtg ggc 883
 Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His Leu Trp Lys Val Gly
 250 255 260

 cag cac aag cgc cac ctc cct gct acc ccg cag gaa aat tgg tgg cgt 931
 Gln His Lys Arg His Leu Pro Ala Thr Pro Gln Glu Asn Trp Trp Arg
 265 270 275

 taatccaaca gtttgagtgt cgc 954

<210> 608

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 608

Met Thr Asn Thr Gln Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro
 1 5 10 15

 Ala Ile Asp Val Ala Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val
 20 25 30

 Asp Tyr Leu Arg Ala Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser
 35 40 45

 Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val
 50 55 60

 Glu Arg Ile Arg Ala Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala
 65 70 75 80

```
<210> 609
<211> 1461
<212> DNA
<213> Corynebacterium glutamicum
```

```

<400> 609
attatgaagc catcggagtt ggtgtggcct acaagggtga tcatgcgtgg atagtgggtgg 60
agttcactgt agtctccgct gattccgtag aatcaacaga gtg aat acc aat ccg 115
                                     Val Asn Thr Asn Pro
                                     1                               5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
                10                15                20

```

gag	ctg	acc	atg	ctt	caa	gca	gcg	ctc	gct	gat	ggg	tct	gca	gaa	cgc	211
Glu	Leu	Thr	Met	Leu	Gln	Ala	Ala	Leu	Ala	Asp	Gly	Ser	Ala	Glu	Arg	
			25					30					35			
ccc	tca	acg	ttt	gag	gtc	ttt	agc	cgc	cgc	ctc	ccc	aac	gag	cgc	cga	259
Pro	Ser	Thr	Phe	Glu	Val	Phe	Ser	Arg	Arg	Leu	Pro	Asn	Glu	Arg	Arg	
		40					45					50				
tac	ggg	gtc	gtc	gca	gga	aca	gca	cga	gtg	ctg	aag	gcg	att	cgt	gac	307
Tyr	Gly	Val	Val	Ala	Gly	Thr	Ala	Arg	Val	Leu	Lys	Ala	Ile	Arg	Asp	
	55					60					65					
ttt	gta	ttc	aca	gag	gaa	caa	ctc	gcc	gat	ctt	gac	ttt	tta	gac	gac	355
Phe	Val	Phe	Thr	Glu	Glu	Gln	Leu	Ala	Asp	Leu	Asp	Phe	Leu	Asp	Asp	
	70					75				80					85	
cgt	acc	ctg	gaa	tac	ctc	cgc	aac	tac	cga	ttc	acc	ggc	caa	gtt	gat	403
Arg	Thr	Leu	Glu	Tyr	Leu	Arg	Asn	Tyr	Arg	Phe	Thr	Gly	Gln	Val	Asp	
				90				95						100		
ggc	tac	cgc	gaa	ggc	gaa	atc	tac	ttc	ccg	cag	tcc	cct	ctt	ctg	act	451
Gly	Tyr	Arg	Glu	Gly	Glu	Ile	Tyr	Phe	Pro	Gln	Ser	Pro	Leu	Leu	Thr	
			105					110					115			
gtg	cgt	ggc	acg	ttt	gca	gaa	tgc	gtc	atc	cta	gaa	act	gtc	att	ttg	499
Val	Arg	Gly	Thr	Phe	Ala	Glu	Cys	Val	Ile	Leu	Glu	Thr	Val	Ile	Leu	
		120					125					130				
tcc	atc	atg	aat	gca	gat	tct	gcc	gtc	gct	tcc	gcc	gct	gcg	cgc	atg	547
Ser	Ile	Met	Asn	Ala	Asp	Ser	Ala	Val	Ala	Ser	Ala	Ala	Ala	Arg	Met	
	135					140					145					
gtc	acc	gca	gct	gat	ggg	cgc	ccc	atc	atc	gaa	atg	gga	tcc	agg	cgc	595
Val	Thr	Ala	Ala	Asp	Gly	Arg	Pro	Ile	Ile	Glu	Met	Gly	Ser	Arg	Arg	
	150				155					160					165	
acc	cac	gaa	tac	tcg	gca	gtc	acc	gca	tcc	cgc	gca	gca	tac	ctc	gct	643
Thr	His	Glu	Tyr	Ser	Ala	Val	Thr	Ala	Ser	Arg	Ala	Ala	Tyr	Leu	Ala	
				170				175						180		
gga	ttc	tcc	acc	acc	tcc	aac	ctc	gag	gcg	gcc	tac	cgc	tac	gga	att	691
Gly	Phe	Ser	Thr	Thr	Ser	Asn	Leu	Glu	Ala	Ala	Tyr	Arg	Tyr	Gly	Ile	
			185				190						195			
cca	gca	tcc	gga	acc	tcc	gcc	cac	gca	tgg	act	ttg	ctg	cac	atc	aac	739
Pro	Ala	Ser	Gly	Thr	Ser	Ala	His	Ala	Trp	Thr	Leu	Leu	His	Ile	Asn	
		200				205						210				
gat	gac	ggc	acc	ccc	aac	gaa	gca	gca	gct	ttc	aaa	gca	cag	gtt	gaa	787
Asp	Asp	Gly	Thr	Pro	Asn	Glu	Ala	Ala	Ala	Phe	Lys	Ala	Gln	Val	Glu	
	215					220					225					
tcc	ctc	ggc	gtg	gac	acc	acc	ttg	ctg	gta	gat	act	tat	gac	atc	acc	835
Ser	Leu	Gly	Val	Asp	Thr	Thr	Leu	Leu	Val	Asp	Thr	Tyr	Asp	Ile	Thr	
	230				235					240					245	
caa	ggg	gtg	gcc	acc	gcc	att	gaa	gtt	gca	ggg	cca	gac	ctt	ggg	ggc	883
Gln	Gly	Val	Ala	Thr	Ala	Ile	Glu	Val	Ala	Gly	Pro	Asp	Leu	Gly	Gly	
			250					255					260			
gta	cgt	atc	gac	tcc	ggc	gac	cta	ggg	gtg	ctt	gcc	cga	aag	gtc	cgc	931

Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg
 265 270 275
 aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc 979
 Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser
 280 285 290
 tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt
 1027
 Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val
 295 300 305
 gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca
 1075
 Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro
 310 315 320 325
 acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg
 1123
 Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val
 330 335 340
 gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct
 1171
 Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala
 345 350 355
 gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac
 1219
 Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr
 360 365 370
 cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc
 1267
 Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser
 375 380 385
 ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct
 1315
 Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro
 390 395 400 405
 act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta
 1363
 Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu
 410 415 420
 cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act
 1411
 Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr
 425 430 435
 cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca
 1458
 Arg Phe Val Gly Phe Pro Pro Ala Ala
 440 445
 aac
 1461

<210> 610
 <211> 446
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 610

```

Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu
  1              5              10              15

Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp
      20              25              30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
      35              40              45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
      50              55              60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
      65              70              75              80

Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
      85              90              95

Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
      100              105              110

Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
      115              120              125

Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
      130              135              140

Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
      145              150              155              160

Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
      165              170              175

Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
      180              185              190

Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
      195              200              205

Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
      210              215              220

Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
      225              230              235              240

Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
      245              250              255

Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu
      260              265              270

Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr
      275              280              285

Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu
  
```

290					295					300					
Arg	Gly	Glu	Pro	Val	Asp	Val	Phe	Gly	Val	Gly	Thr	Ser	Val	Val	Thr
305					310					315					320
Gly	Ser	Gly	Ala	Pro	Thr	Ala	Gly	Leu	Val	Tyr	Lys	Ile	Gly	Glu	Val
				325					330					335	
Ala	Gly	His	Pro	Val	Ala	Lys	Arg	Ser	Arg	Asn	Lys	Glu	Ser	Tyr	Gly
			340					345					350		
Gly	Gly	Lys	Lys	Ala	Val	Arg	Thr	His	Arg	Lys	Ser	Gly	Thr	Ala	Ile
		355					360					365			
Glu	Glu	Ile	Val	Tyr	Pro	Phe	Asn	Ala	Glu	Ala	Pro	Asp	Thr	Gly	Lys
	370					375					380				
Leu	Asp	Thr	Leu	Ser	Leu	Thr	Ile	Pro	Leu	Met	Arg	Asp	Gly	Glu	Ile
385					390					395					400
Val	Pro	Gly	Leu	Pro	Thr	Leu	Glu	Asp	Ser	Arg	Ala	Tyr	Leu	Ala	Lys
				405					410					415	
Gln	Leu	Val	Ser	Leu	Pro	Trp	Glu	Gly	Leu	Ala	Leu	Ser	Arg	Asp	Glu
			420					425					430		
Pro	Val	Leu	His	Thr	Arg	Phe	Val	Gly	Phe	Pro	Pro	Ala	Ala		
		435					440					445			

<210> 611

<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> RXA02299

<400> 611

acgcgggggt tgttgccgga tcgaaatatt cctttccttg tcattctcacg ctatgatttc 60

taaaacttgc	aggacaaccc	ccataaggac	accacaggac	atg	ctg	cgc	acc	atc	115
				Met	Leu	Arg	Thr	Ile	
				1				5	

ctc	gga	agt	aag	att	cac	cga	gcc	act	gtc	act	caa	gct	gat	cta	gat	163
Leu	Gly	Ser	Lys	Ile	His	Arg	Ala	Thr	Val	Thr	Gln	Ala	Asp	Leu	Asp	
				10					15					20		

tat	gtt	ggc	tct	gta	acc	atc	gac	gcc	gac	ctg	gtt	cac	gcc	gcc	gga	211
Tyr	Val	Gly	Ser	Val	Thr	Ile	Asp	Ala	Asp	Leu	Val	His	Ala	Ala	Gly	
			25					30					35			

ttg	atc	gaa	ggc	gaa	aaa	gtt	gcc	atc	gta	gac	atc	acc	aac	ggc	gct	259
Leu	Ile	Glu	Gly	Glu	Lys	Val	Ala	Ile	Val	Asp	Ile	Thr	Asn	Gly	Ala	
		40					45					50				

cgt	ctg	gaa	act	tat	gtc	att	gtg	ggc	gac	gcc	gga	acg	ggc	aat	att	307
Arg	Leu	Glu	Thr	Tyr	Val	Ile	Val	Gly	Asp	Ala	Gly	Thr	Gly	Asn	Ile	

55 60 65

tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg 355
 Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val
 70 75 80 85

atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat 403
 Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr
 90 95 100

gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc 451
 Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu
 105 110 115

ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg 499
 Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser
 120 125 130

aga agc att tagcgtttta gctcgccaat att 531
 Arg Ser Ile
 135

<210> 612

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 612

Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr
 1 5 10 15

Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu
 20 25 30

Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp
 35 40 45

Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala
 50 55 60

Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn
 65 70 75 80

Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala
 85 90 95

Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn
 100 105 110

Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser
 115 120 125

Gly Leu Leu Thr Ser Arg Ser Ile
 130 135

<210> 613

<211> 960

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(937)

<223> RXA01928

<400> 613

gcgagtacgc caccttgggc gattccttgc acgacgccgc gcaggcctac atcgccgata 60

tccacgcggg taccttccca ggcgaagcgg agtcctttta atg cag gta gca acc 115
 Met Gln Val Ala Thr
 1 5

aca aag cag gcg ctt atc gac gcc ctc ctc cac cac aaa tcc gtc ggg 163
 Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His His Lys Ser Val Gly
 10 15 20

ctc gtc ccc acc atg ggt gcg cta cac agc gga cac gcc tcg ttg gtt 211
 Leu Val Pro Thr Met Gly Ala Leu His Ser Gly His Ala Ser Leu Val
 25 30 35

aaa gca gca cgc gct gaa aac gac act gtt gta gcc agt att ttt gtc 259
 Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val Ala Ser Ile Phe Val
 40 45 50

aat ccc ctg cag ttt gaa gca ctc ggt gat tgc gat gat tac cgc aac 307
 Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys Asp Asp Tyr Arg Asn
 55 60 65

tat ccc cgc caa ctc gac gcc gat tta gca ctg ctt gaa gag gca ggt 355
 Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu Leu Glu Glu Ala Gly
 70 75 80 85

gtg gat att gtg ttc gca ccc gat gtg gag gaa atg tac ccc ggt ggc 403
 Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu Met Tyr Pro Gly Gly
 90 95 100

ttg cca cta gtg tgg gcg cgc acc ggt tcc atc gga aca aaa ttg gag 451
 Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile Gly Thr Lys Leu Glu
 105 110 115

ggt gcc agc agg cct ggc cat ttc gat ggt gtg gct acc gtg gtg gcg 499
 Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val Ala Thr Val Val Ala
 120 125 130

aag ctg ttc aat ttg gtg cgc cct gat cgt gca tat ttt gga caa aaa 547
 Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala Tyr Phe Gly Gln Lys
 135 140 145

gat gct cag cag gtt gcg gtg att cgg cga ttg gtt gcc gat cta gac 595
 Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu Val Ala Asp Leu Asp
 150 155 160 165

att ccc gtg gag att cgt ccc gtt ccg att att cgt ggc gcc gat ggc 643
 Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile Arg Gly Ala Asp Gly
 170 175 180

tta gcc gaa tcc agc cgc aat caa cgt ctt tct gcg gat cag cga gcg 691
 Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser Ala Asp Gln Arg Ala
 185 190 195

caa gct ctg gtg ctg ccg cag gtg ttg agt ggg ttg cag cgt cga aaa 739
 Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly Leu Gln Arg Arg Lys
 200 205 210
 gca gct ggt gaa gcg cta gat atc caa ggt gcg cgc gac acc ttg gcc 787
 Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala Arg Asp Thr Leu Ala
 215 220 225
 agc gcc gac ggc gtg cgc ttg gat cac ctg gaa att gtc gat cca gcc 835
 Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu Ile Val Asp Pro Ala
 230 235 240 245
 acc ctc gaa cca tta gaa atc gac ggc ctg ctc acc caa cca gcg ttg 883
 Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu Thr Gln Pro Ala Leu
 250 255 260
 gtg gtc ggc gcg att ttc gtg ggg ccg gtg cgg ttg atc gac aat atc 931
 Val Val Gly Ala Ile Phe Val Gly Pro Val Arg Leu Ile Asp Asn Ile
 265 270 275
 gag ctc tagtaccaac cctgcgttgc agc 960
 Glu Leu

<210> 614

<211> 279

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 614

Met Gln Val Ala Thr Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His
 1 5 10 15
 His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser Gly
 20 25 30
 His Ala Ser Leu Val Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val
 35 40 45
 Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys
 50 55 60
 Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu
 65 70 75 80
 Leu Glu Glu Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu
 85 90 95
 Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile
 100 105 110
 Gly Thr Lys Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val
 115 120 125
 Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala
 130 135 140
 Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu
 145 150 155 160

Val Ala Asp Leu Asp Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile
 165 170 175

Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser
 180 185 190

Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly
 195 200 205

Leu Gln Arg Arg Lys Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala
 210 215 220

Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu
 225 230 235 240

Ile Val Asp Pro Ala Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu
 245 250 255

Thr Gln Pro Ala Leu Val Val Gly Ala Ile Phe Val Gly Pro Val Arg
 260 265 270

Leu Ile Asp Asn Ile Glu Leu
 275

<210> 615
 <211> 936
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(913)
 <223> RXN01929

<400> 615
 aaaatttgac tccataacga gaacttaatc gagcaacacc cctgaacagt gaatcaaadc 60

ggaattttatt tattctgagc tggatcatcac atctataactc atg ccc atg tca ggc 115
 Met Pro Met Ser Gly
 1 5

att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163
 Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val
 10 15 20

aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala
 25 30 35

cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259
 Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser
 40 45 50

gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307
 Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu
 55 60 65

gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355
 Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg
 70 75 80 85

gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403
Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro
90 95 100

aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451
Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala
105 110 115

gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499
Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg
120 125 130

cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547
Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr
135 140 145

ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595
Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly
150 155 160 165

gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643
Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala
170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691
Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg
185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739
Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly
200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787
Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu
215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835
Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly
230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883
Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala
250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933
Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
265 270

aag 936

<210> 616

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 616

Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe
1 5 10 15

Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr
 20 25 30
 Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu
 35 40 45
 Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr
 50 55 60
 Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr
 65 70 75 80
 Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr
 85 90 95
 Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met
 100 105 110
 Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile
 115 120 125
 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly
 130 135 140
 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val
 145 150 155 160
 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg
 165 170 175
 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro
 180 185 190
 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile
 195 200 205
 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln
 210 215 220
 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu
 225 230 235 240
 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile
 245 250 255
 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265 270

<210> 617

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> FRXA01929

<400> 617

tgactccata acgagaactt aatcgagcaa caccctgaa cagtgaatca aatcggaatt 60

tattttattct gagctgggtca tcacatctat actcatgccc atg tca ggc att gat	115
Met Ser Gly Ile Asp	
1 5	
gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly	
10 15 20	
cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile	
25 30 35	
ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala	
40 45 50	
aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu	
55 60 65	
atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355
Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu	
70 75 80 85	
gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag	403
Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln	
90 95 100	
gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg gct gcg	451
Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala	
105 110 115	
gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att	499
Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile	
120 125 130	
gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag	547
Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln	
135 140 145	
tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt	595
Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser	
150 155 160 165	
tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg	643
Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala	
170 175 180	
ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt	691
Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val	
185 190 195	
acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc	739
Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly	
200 205 210	
aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc	787
Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg	
215 220 225	

ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835
 Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser
 230 235 240 245
 ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883
 Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr
 250 255 260
 ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930
 Phe Pro Gly Glu Ala Glu Ser Phe
 265

<210> 618

<211> 269

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 618

Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu
 1 5 10 15
 Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala
 20 25 30
 Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val
 35 40 45
 Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser
 50 55 60
 Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala
 65 70 75 80
 Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu
 85 90 95
 Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu
 100 105 110
 Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln
 115 120 125
 Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile
 130 135 140
 Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln
 145 150 155 160
 Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu
 165 170 175
 Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu
 180 185 190
 Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile
 195 200 205
 Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala
 210 215 220

Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala
225 230 235 240

Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp
245 250 255

Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
260 265

<210> 619

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXA01521

<400> 619

```

acccccggcag gcaacgcctt ttccgggatt tggcgcgag gcaggcagag atttcccgcg 60
cgcaagatat tgagctgtgg gcaattcaga aggaggaccg ttg agt ttc acg cat 115
                                Leu Ser Phe Thr His
                                1 5

ggt cag ggc aga gtt ttt gat acc gtc gag cag atc cgc atg ttc ggc 163
Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln Ile Arg Met Phe Gly
                                10 15 20

agc gcc ctg cgc aaa acc ggc aaa cca gtg gtg ctc gta ccc ttg gga 211
Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val Leu Val Pro Leu Gly
                                25 30 35

aat ggc ctc cac gca ggc cat att gcg ctc atc cgc gca gca aaa cgc 259
Asn Gly Leu His Ala Gly His Ile Ala Leu Ile Arg Ala Ala Lys Arg
                                40 45 50

atc ccc ggt gcg gtg gtc gtc gtc gcc tat gcc ggc ccg gaa tcg gat 307
Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala Gly Pro Glu Ser Asp
                                55 60 65

cac gca cgt tta agg gaa gag ctt atc gac gcg atc ttc ccg ttc aat 355
His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala Ile Phe Pro Phe Asn
                                70 75 80 85

ccc gaa acg cta tgg cct cac ggc atc cgg gtg gaa gtt aca ggt ggc 403
Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val Glu Val Thr Gly Gly
                                90 95 100

cca aca ctt acc cca caa ggt gcg gaa gta acc aag gtg ctg ggg ctg 451
Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr Lys Val Leu Gly Leu
                                105 110 115

ttg gga atc acc gga gca act gat gtg gtg ctc ggt gaa aag gac tat 499
Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu Gly Glu Lys Asp Tyr
                                120 125 130

gag ctg gtg gtt cta gtc cag cgc gcc ctt aat gat ctg cat att cca 547
Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn Asp Leu His Ile Pro

```

135	140	145	
gta aaa ctg cat tct gtt cca acc gtg cgc atg cca gat gga cta gcc			595
Val Lys Leu His Ser Val Pro Thr Val Arg Met Pro Asp Gly Leu Ala			
150	155	160	165
att tcc ctg cgt aat att tca gtg ccc gaa gac tcc cgc gaa acg gca			643
Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp Ser Arg Glu Thr Ala			
	170	175	180
ttg agc ctg gca gca gcc ctc acc gcc ggt gcg cat tcg gca gaa cac			691
Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala His Ser Ala Glu His			
	185	190	195
ggc gag gca gtg gtt aaa gaa aca gtc acg caa gtg ctc aaa gcc gca			739
Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln Val Leu Lys Ala Ala			
	200	205	210
ggc gtg acc ccc gat tat gta gaa atc cgt ggc ctg gat ctt gga cca			787
Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly Leu Asp Leu Gly Pro			
	215	220	225
gcc ccc gaa atc gga gac gcc cga ctc ttc gca gcc atc acg ctt ggc			835
Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala Ala Ile Thr Leu Gly			
	230	235	240
gat gtc caa ctc cac gac aac gtc ggc cta ccc ctt gga atc ggc ttc			883
Asp Val Gln Leu His Asp Asn Val Gly Leu Pro Leu Gly Ile Gly Phe			
	250	255	260
aaa aac atc gaa ggc tgatccccggt ttaccagtt cgc			921
Lys Asn Ile Glu Gly			
	265		

<210> 620

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 620

Leu Ser Phe Thr His Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln			
1	5	10	15
Ile Arg Met Phe Gly Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val			
	20	25	30
Leu Val Pro Leu Gly Asn Gly Leu His Ala Gly His Ile Ala Leu Ile			
	35	40	45
Arg Ala Ala Lys Arg Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala			
	50	55	60
Gly Pro Glu Ser Asp His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala			
	65	70	75
Ile Phe Pro Phe Asn Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val			
	85	90	95
Glu Val Thr Gly Gly Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr			
	100	105	110

Lys Val Leu Gly Leu Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu
 115 120 125
 Gly Glu Lys Asp Tyr Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn
 130 135 140
 Asp Leu His Ile Pro Val Lys Leu His Ser Val Pro Thr Val Arg Met
 145 150 155 160
 Pro Asp Gly Leu Ala Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp
 165 170 175
 Ser Arg Glu Thr Ala Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala
 180 185 190
 His Ser Ala Glu His Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln
 195 200 205
 Val Leu Lys Ala Ala Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly
 210 215 220
 Leu Asp Leu Gly Pro Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala
 225 230 235 240
 Ala Ile Thr Leu Gly Asp Val Gln Leu His Asp Asn Val Gly Leu Pro
 245 250 255
 Leu Gly Ile Gly Phe Lys Asn Ile Glu Gly
 260 265

<210> 621

<211> 1137

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1114)

<223> RXS01145

<400> 621

taatgtagtt gtctgccc aa gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60
 cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc
1027

Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc
1075

Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac
1124

Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala
330 335

ccctttgacg gct
1137

<210> 622

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 622

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
 195 200 205
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
 210 215 220
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
 275 280 285
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
 290 295 300
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala
 305 310 315 320
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu
 325 330 335
 Thr Ala

<210> 623
 <211> 556
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(556)
 <223> FRXA01145

<400> 623
 taatgtagtt gtctgcccac gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60
 cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala
55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr
70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala
90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu
105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly
120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro
135 140 145

tgc ctc atc 556
Cys Leu Ile
150

<210> 624

<211> 152

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 624

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile
145 150

<210> 625

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1366)

<223> RXA02239

<400> 625

```

ctatgcacag cggaggtcga gggagagcgt ggggtggcgt cgaaaagcat cttgtagagt 60
gtgtgggaac ccagccagcc tcttactttg aaggattggt gtg ccc atg act cat 115
                               Val Pro Met Thr His
                               1 5

gtt tca agc ccc tcc gca ccc cgc aac gtg gtt gtt ggt gtt gcc ggc 163
Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val Val Gly Val Ala Gly
                               10 15 20

gga atc gca gcg tac aag gcg tgt cac atc gtg cgc gcg ttt aaa gaa 211
Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val Arg Ala Phe Lys Glu
                               25 30 35

gcg ggc gat aat gtg cgg gtg gtt cct acg gaa tcc gcg ttg aag ttt 259
Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu Ser Ala Leu Lys Phe
                               40 45 50

gtg ggg aag gcg acg ttt gaa gcg ttg tct ggc aat ccg gtg tct aca 307
Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly Asn Pro Val Ser Thr
                               55 60 65

acg gtg ttt gat gcg gtg gat tcg gtg cag cat gtg aaa gtt ggc cag 355
Thr Val Phe Asp Ala Val Asp Ser Val Gln His Val Lys Val Gly Gln
                               70 75 80 85

gaa gct gat ttg atc gtg att gcg ccg gcg aca gcc gat ttg atg gcg 403
Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr Ala Asp Leu Met Ala
                               90 95 100

cgt gtg gtg gca ggt ctc ggt gac gat ctg ttg gcg gcg acg ctg ctg 451
Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu Ala Ala Thr Leu Leu
                               105 110 115

gtg gca acg tgc ccc gtg gtt att gcg ccg gcc atg cat acg gag atg 499
Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala Met His Thr Glu Met
                               120 125 130

tgg ttt aat ccg gct acc gta gcc aat gtg gca acg ctg agg cag cgg 547
Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala Thr Leu Arg Gln Arg
                               135 140 145

ggg att acc gtg att gag cct gcg cat ggt cga ctc acc ggt aaa gat 595
Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg Leu Thr Gly Lys Asp
150 155 160 165

```

aca ggc cct ggc cgg ctg ccg gat cca gag cag att gtt gat tta gcc 643
 Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln Ile Val Asp Leu Ala
 170 175 180

aat gcg gtg cac gcc ggg gcg agg ttg cct cag gat ttg gcg ggc aag 691
 Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln Asp Leu Ala Gly Lys
 185 190 195

aaa gtg ctg atc act gct ggt ggc acg cat gag cat att gat cct gtg 739
 Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu His Ile Asp Pro Val
 200 205 210

cgc ttt att ggc aat agt tcc tcg ggc cgt caa ggt ttt gcg ttg ggt 787
 Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln Gly Phe Ala Leu Gly
 215 220 225

gaa atc gca gca cag cga ggt gct cat gtc agc atc gtg gcg gga aat 835
 Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser Ile Val Ala Gly Asn
 230 235 240 245

gct gcg gag ctg ccc act ccg gca ggc gca gag atc gtg ccg gtg gtg 883
 Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu Ile Val Pro Val Val
 250 255 260

tcc aca caa gac atg ttt gat gca gtc cag gaa cga gct ggc caa tct 931
 Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu Arg Ala Gly Gln Ser
 265 270 275

gat ttc atc gtc atg gcg gca gcg gta gct gat ttc acg ccc gca tcg 979
 Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp Phe Thr Pro Ala Ser
 280 285 290

cag gcg aca tcg aag ttg aag aag ggc tca gat tct gat gaa gac gca
 1027
 Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp Ser Asp Glu Asp Ala
 295 300 305

ttg agc acc atc tcg ttg gtg gaa aac ccg gat att ttg gct acc acg
 1075
 Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp Ile Leu Ala Thr Thr
 310 315 320 325

gtg aag cgt cgt gaa gca gga gag ctg gac agt aat cct gtc atc gtg
 1123
 Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser Asn Pro Val Ile Val
 330 335 340

ggt ttt gct gcg gaa act gga gac gag cac acc acc gcc ttg gag tat
 1171
 Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr Thr Ala Leu Glu Tyr
 345 350 355

gcg cgc aag aaa ctg cag aag aag ggc tgc gac ctc ctc atg tgt aat
 1219
 Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp Leu Leu Met Cys Asn
 360 365 370

gag gtg ggc atg ggc aaa gtg ttt ggg caa aag cac aat gag ggc tgg
 1267
 Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys His Asn Glu Gly Trp
 375 380 385

att ttg gat gct cac ggt ggg gta gtc gat gtg gag cac ggc agc aaa
 1315
 Ile Leu Asp Ala His Gly Gly Val Val Asp Val Glu His Gly Ser Lys
 390 395 400 405

atc gag gtt gct gcg caa att tgg gac gcg gca ctg gcg tat cgc gaa
 1363
 Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala Leu Ala Tyr Arg Glu
 410 415 420

gtc tagaaaaatc cagctagacc act
 1389
 Val

<210> 626
 <211> 422
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 626
 Val Pro Met Thr His Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val
 1 5 10 15
 Val Gly Val Ala Gly Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val
 20 25 30
 Arg Ala Phe Lys Glu Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu
 35 40 45
 Ser Ala Leu Lys Phe Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly
 50 55 60
 Asn Pro Val Ser Thr Thr Val Phe Asp Ala Val Asp Ser Val Gln His
 65 70 75 80
 Val Lys Val Gly Gln Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr
 85 90 95
 Ala Asp Leu Met Ala Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu
 100 105 110
 Ala Ala Thr Leu Leu Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala
 115 120 125
 Met His Thr Glu Met Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala
 130 135 140
 Thr Leu Arg Gln Arg Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg
 145 150 155 160
 Leu Thr Gly Lys Asp Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln
 165 170 175
 Ile Val Asp Leu Ala Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln
 180 185 190
 Asp Leu Ala Gly Lys Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu
 195 200 205

His Ile Asp Pro Val Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln
 210 215 220
 Gly Phe Ala Leu Gly Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser
 225 230 235 240
 Ile Val Ala Gly Asn Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu
 245 250 255
 Ile Val Pro Val Val Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu
 260 265 270
 Arg Ala Gly Gln Ser Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp
 275 280 285
 Phe Thr Pro Ala Ser Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp
 290 295 300
 Ser Asp Glu Asp Ala Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp
 305 310 315 320
 Ile Leu Ala Thr Thr Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser
 325 330 335
 Asn Pro Val Ile Val Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr
 340 345 350
 Thr Ala Leu Glu Tyr Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp
 355 360 365
 Leu Leu Met Cys Asn Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys
 370 375 380
 His Asn Glu Gly Trp Ile Leu Asp Ala His Gly Gly Val Val Asp Val
 385 390 395 400
 Glu His Gly Ser Lys Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala
 405 410 415
 Leu Ala Tyr Arg Glu Val
 420

<210> 627

<211> 1092

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1069)

<223> RXA00581

<400> 627

gcatgagttt actcacgtgc ccacgtcttt tagccacca ttgaagtga aaaataaccc 60

 cgatcacact agtggagtag ctaagggtgca caatggattc atg gca gag caa aac 115
 Met Ala Glu Gln Asn
 1 5

gct gca agc aca act ggt gtg aaa cct tcc cca cgc aca cca gat ttc	163
Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro Arg Thr Pro Asp Phe	
10 15 20	
agc ccc tac ctt gat ttc gac cgc gca caa tgg cgc gag ctg aga aac	211
Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp Arg Glu Leu Arg Asn	
25 30 35	
tca atg cct cag gtg ctg acc caa aaa gaa gtc att gaa ctt cga ggc	259
Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val Ile Glu Leu Arg Gly	
40 45 50	
atc gga gaa aac att gac ctc gct gaa gtg gca gaa gtc tac ctt ccg	307
Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala Glu Val Tyr Leu Pro	
55 60 65	
ctg tcc cgt ctg att cac ctc cag gta gcg gcc cga cag caa ctt act	355
Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala Arg Gln Gln Leu Thr	
70 75 80 85	
gca gcc acc gaa acc ttc ctc gga act tcc ccc tct atc tct gtg ccg	403
Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro Ser Ile Ser Val Pro	
90 95 100	
ttt gtc att ggt gtc gcg gga tcc gtc gcc gtc ggt aaa tca acc acc	451
Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr	
105 110 115	
gcc cga ctc ctc caa gtt ctg ctt cag cgc tgg aat tcc cac ccc cgc	499
Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp Asn Ser His Pro Arg	
120 125 130	
gtg gac ctc gtc acc acc gac gga ttc ctc tat ccc ggc gcg gaa cta	547
Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr Pro Gly Ala Glu Leu	
135 140 145	
atc cgc cgc gga tta atg tcc cga aaa gga ttc ccc gaa agc tac gac	595
Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp	
150 155 160 165	
caa cgt gca ctc ctc cgc ttt gtc acc gac gta aaa tcc gga aaa ctc	643
Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val Lys Ser Gly Lys Leu	
170 175 180	
gaa gtc aac gca cct gtc tac tcc cac acc gcg tac gac cga gtt cca	691
Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala Tyr Asp Arg Val Pro	
185 190 195	
ggc gaa ttc acc aca gtc cgc caa ccc gac att ttg atc gtc gaa ggc	739
Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile Leu Ile Val Glu Gly	
200 205 210	
tta aac gtc ctc caa act ggc cca aca ttg atg gtc agt gac ctt ttc	787
Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met Val Ser Asp Leu Phe	
215 220 225	
gac ttc agc gtc tac gta gat gcc cgc acc gaa gat atc gaa aaa tgg	835
Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu Asp Ile Glu Lys Trp	
230 235 240 245	
tac atc gac cgc ttc ctc aaa ctc cgc gac act gca ttc cgt cgc ccc	883

Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr Ala Phe Arg Arg Pro
 250 255 260
 ggt gcc cac ttc tcc cat tac gcc gac atg gct gat cca gag tcc atc 931
 Gly Ala His Phe Ser His Tyr Ala Asp Met Ala Asp Pro Glu Ser Ile
 265 270 275
 gcc gtc gct cga gaa ctg tgg caa tcg atc aac ctg ccc aac ttg gtg 979
 Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn Leu Pro Asn Leu Val
 280 285 290
 gag aat att ctt ccc acc cga gtt cgc gcg tcg ttg gta ctg aaa aaa
 1027
 Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser Leu Val Leu Lys Lys
 295 300 305
 ggt agc gat cac ttg gtg gaa cgg gtg agg atg cgc aag atc
 1069
 Gly Ser Asp His Leu Val Glu Arg Val Arg Met Arg Lys Ile
 310 315 320
 taggggttct tgctggtttt gag
 1092
 <210> 628
 <211> 323
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 628
 Met Ala Glu Gln Asn Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro
 1 5 10 15
 Arg Thr Pro Asp Phe Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp
 20 25 30
 Arg Glu Leu Arg Asn Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val
 35 40 45
 Ile Glu Leu Arg Gly Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala
 50 55 60
 Glu Val Tyr Leu Pro Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala
 65 70 75 80
 Arg Gln Gln Leu Thr Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro
 85 90 95
 Ser Ile Ser Val Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val
 100 105 110
 Gly Lys Ser Thr Thr Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp
 115 120 125
 Asn Ser His Pro Arg Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr
 130 135 140
 Pro Gly Ala Glu Leu Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe
 145 150 155 160

Pro Glu Ser Tyr Asp Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val
 165 170 175

Lys Ser Gly Lys Leu Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala
 180 185 190

Tyr Asp Arg Val Pro Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile
 195 200 205

Leu Ile Val Glu Gly Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met
 210 215 220

Val Ser Asp Leu Phe Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu
 225 230 235 240

Asp Ile Glu Lys Trp Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr
 245 250 255

Ala Phe Arg Arg Pro Gly Ala His Phe Ser His Tyr Ala Asp Met Ala
 260 265 270

Asp Pro Glu Ser Ile Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn
 275 280 285

Leu Pro Asn Leu Val Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser
 290 295 300

Leu Val Leu Lys Lys Gly Ser Asp His Leu Val Glu Arg Val Arg Met
 305 310 315 320

Arg Lys Ile

<210> 629
 <211> 1023
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1000)
 <223> RXS00838

<400> 629
 tcgtctaata gtgctgccaa tccaccggcc attgatgact cctttgtaga gaaggggtag 60

tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115
 Met Lys Ile Ala Ile
 1 5

gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu
 10 15 20

tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211
 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala
 25 30 35

ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr

40	45	50	
gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp 55 60 65			307
gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala 70 75 80 85			355
gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln 90 95 100			403
aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp 105 110 115			451
cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro 120 125 130			499
gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp 135 140 145			547
tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly 150 155 160 165			595
att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys 170 175 180			643
gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys 185 190 195			691
caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu 200 205 210			739
atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro 215 220 225			787
agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu 230 235 240 245			835
aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser 250 255 260			883
gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val 265 270 275			931
ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu 280 285 290			979

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg

1023

Lys Glu Glu Glu Asn Ser Leu

295

300

<210> 630

<211> 300

<212> PRT

<213> Corynebacterium glutamicum

<400> 630

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly
1 5 10 15

Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly
20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala
35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu
50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg
65 70 75 80

Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val
85 90 95

Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys
100 105 110

Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe
115 120 125

Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser
130 135 140

Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr
145 150 155 160

Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val
165 170 175

Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly
180 185 190

Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala
195 200 205

Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala
210 215 220

Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala
225 230 235 240

Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala
245 250 255

Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg
260 265 270

Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr
275 280 285

Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu
290 295 300

<210> 631

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> RXC02238

<400> 631

```

ggcgcttagc caaaacatag agcggtaggg tatgcttattc cgattgagca acctttcccg 60
ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
                               Val Thr Asn Val Ser
                               1 5
aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
                10                15                20
acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
                25                30                35
gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
                40                45                50
tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
                55                60                65
act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
                70                75                80                85
aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
                90                95
cac 408

```

<210> 632

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 632

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp

1	5	10	15
Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys	20	25	30
Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg	35	40	45
Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe	50	55	60
Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile	65	70	75
Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly	85	90	95
<210> 633			
<211> 606			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(583)			
<223> RXN03058			
<400> 633			
acgagcttcc gctctgcaca agccgctaga agccccgcat agccctaata tagagctcat 60			
gccatttgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa 115			
Val Ser Lys Leu Lys 1 5			
ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163			
Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala 10 15 20			
gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211			
Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu 25 30 35			
att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259			
Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala 40 45 50			
atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307			
Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu 55 60 65			
aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355			
Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val 70 75 80 85			
ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403			
Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu 90 95 100			
caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451			
Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln			

105 110 115
 atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499
 Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile
 120 125 130
 cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547
 Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly
 135 140 145
 atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593
 Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro
 150 155 160
 tataaaccaa aaa 606

<210> 634
 <211> 161
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 634
 Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly
 1 5 10 15
 Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp
 20 25 30
 Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr
 35 40 45
 Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
 50 55 60
 Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
 65 70 75 80
 Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
 85 90 95
 Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile
 100 105 110
 Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
 115 120 125
 Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
 130 135 140
 Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys
 145 150 155 160
 Pro

<210> 635
 <211> 606
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(583)

<223> FRXA02903

<400> 635

```

acgagcttcc gctctgcaca agccgctaga agccccgcat agccctaattg tagagctcat 60
gcccatattgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa 115
                                         Val Ser Lys Leu Lys
                                         1 5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163
Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala
                        10 15 20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211
Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu
                        25 30 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259
Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala
                        40 45 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307
Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu
                        55 60 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355
Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val
                        70 75 80 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403
Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu
                        90 95 100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451
Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln
                        105 110 115

atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499
Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile
                        120 125 130

cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly
                        135 140 145

atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593
Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro
150 155 160

tataaaccaa aaa 606

```

<210> 636

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 636

Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly
 1 5 10 15

Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp
 20 25 30

Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr
 35 40 45

Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
 50 55 60

Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
 65 70 75 80

Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
 85 90 95

Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile
 100 105 110

Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
 115 120 125

Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
 130 135 140

Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys
 145 150 155 160

Pro

<210> 637

<211> 783

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(760)

<223> RXA00166

<400> 637

ggcgttttagc gatcttcaac atcgagcaac cagcgccagc gcttttacc aaggcagcac 60

gacttatcac gatgtccgac ctggatatcc ggctgaggcc gtg gag tta gcc cgt 115
 Val Glu Leu Ala Arg
 1 5

ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc 163
 Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr
 10 15 20

agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac 211
 Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp
 25 30 35

atg ttg cgg gtg ttt cgc tcc gcg ctt ccg gcg gtt ccc tgc tgg caa 259

Met	Leu	Arg	Val	Phe	Arg	Ser	Ala	Leu	Pro	Ala	Val	Pro	Cys	Trp	Gln	
		40					45					50				
gcg	aca	gca	gaa	cac	aca	gga	ata	cgt	gac	aac	gcg	gtt	gat	ctg	att	307
Ala	Thr	Ala	Glu	His	Thr	Gly	Ile	Arg	Asp	Asn	Ala	Val	Asp	Leu	Ile	
	55					60				65						
acg	tgc	gca	caa	acg	tgg	cat	tgg	gtt	gac	gtg	acg	gct	gcc	tca	gcg	355
Thr	Cys	Ala	Gln	Thr	Trp	His	Trp	Val	Asp	Val	Thr	Ala	Ala	Ser	Ala	
	70				75				80					85		
gaa	ttt	gat	cgg	gtg	att	gca	cct	gag	ggc	gca	gtc	ctg	ctc	gtg	tgg	403
Glu	Phe	Asp	Arg	Val	Ile	Ala	Pro	Glu	Gly	Ala	Val	Leu	Leu	Val	Trp	
				90					95					100		
aat	aac	ctg	gac	acc	tcc	atc	gcg	tgg	gta	cac	cga	ctc	agt	cgc	att	451
Asn	Asn	Leu	Asp	Thr	Ser	Ile	Ala	Trp	Val	His	Arg	Leu	Ser	Arg	Ile	
			105					110					115			
atg	cat	gcc	ggc	gat	gta	ctc	aag	ccg	gga	ttc	acc	cca	gaa	acc	gca	499
Met	His	Ala	Gly	Asp	Val	Leu	Lys	Pro	Gly	Phe	Thr	Pro	Glu	Thr	Ala	
		120					125					130				
gct	ccc	tgg	ata	att	gat	cga	gaa	att	cgc	acc	acg	tgg	aat	cag	cac	547
Ala	Pro	Trp	Ile	Ile	Asp	Arg	Glu	Ile	Arg	Thr	Thr	Trp	Asn	Gln	His	
	135					140					145					
ctc	acc	cct	gaa	gaa	atc	atc	cag	ctc	gct	cac	acg	agg	tcc	tac	tgg	595
Leu	Thr	Pro	Glu	Glu	Ile	Ile	Gln	Leu	Ala	His	Thr	Arg	Ser	Tyr	Trp	
	150				155					160					165	
tta	aac	gcg	tca	gag	aaa	atc	aaa	gag	cgt	gtt	gat	cag	aac	ctt	cag	643
Leu	Asn	Ala	Ser	Glu	Lys	Ile	Lys	Glu	Arg	Val	Asp	Gln	Asn	Leu	Gln	
				170				175						180		
tgg	tat	ctc	tac	gag	cat	ttg	ggc	ttc	agt	ccc	gac	aat	cca	gtg	gaa	691
Trp	Tyr	Leu	Tyr	Glu	His	Leu	Gly	Phe	Ser	Pro	Asp	Asn	Pro	Val	Glu	
			185				190						195			
ctt	ccc	tat	cgc	tgt	gat	gca	ttt	tta	ctt	tca	cgt	tcc	ggc	acc	ctg	739
Leu	Pro	Tyr	Arg	Cys	Asp	Ala	Phe	Leu	Leu	Ser	Arg	Ser	Gly	Thr	Leu	
		200				205						210				
gca	ggc	aga	tct	tcc	aat	ctt	taggagccct	cgccatgtac	ctg							783
Ala	Gly	Arg	Ser	Ser	Asn	Leu										
	215					220										

<210> 638

<211> 220

<212> PRT

<213> Corynebacterium glutamicum

<400> 638

Val	Glu	Leu	Ala	Arg	Gly	Phe	Gly	Arg	Val	Leu	Asp	Val	Gly	Ala	Gly
1				5					10					15	

Thr	Gly	Lys	Leu	Thr	Ser	Glu	Leu	Thr	Ala	Asp	Gln	Val	Leu	Ala	Leu
		20						25					30		

Asp	Pro	Ser	Met	Asp	Met	Leu	Arg	Val	Phe	Arg	Ser	Ala	Leu	Pro	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35					40					45					
Val	Pro	Cys	Trp	Gln	Ala	Thr	Ala	Glu	His	Thr	Gly	Ile	Arg	Asp	Asn
50						55					60				
Ala	Val	Asp	Leu	Ile	Thr	Cys	Ala	Gln	Thr	Trp	His	Trp	Val	Asp	Val
65					70					75					80
Thr	Ala	Ala	Ser	Ala	Glu	Phe	Asp	Arg	Val	Ile	Ala	Pro	Glu	Gly	Ala
				85					90					95	
Val	Leu	Leu	Val	Trp	Asn	Asn	Leu	Asp	Thr	Ser	Ile	Ala	Trp	Val	His
			100					105					110		
Arg	Leu	Ser	Arg	Ile	Met	His	Ala	Gly	Asp	Val	Leu	Lys	Pro	Gly	Phe
		115					120					125			
Thr	Pro	Glu	Thr	Ala	Ala	Pro	Trp	Ile	Ile	Asp	Arg	Glu	Ile	Arg	Thr
	130					135					140				
Thr	Trp	Asn	Gln	His	Leu	Thr	Pro	Glu	Glu	Ile	Ile	Gln	Leu	Ala	His
145					150					155					160
Thr	Arg	Ser	Tyr	Trp	Leu	Asn	Ala	Ser	Glu	Lys	Ile	Lys	Glu	Arg	Val
				165					170					175	
Asp	Gln	Asn	Leu	Gln	Trp	Tyr	Leu	Tyr	Glu	His	Leu	Gly	Phe	Ser	Pro
			180					185					190		
Asp	Asn	Pro	Val	Glu	Leu	Pro	Tyr	Arg	Cys	Asp	Ala	Phe	Leu	Leu	Ser
		195					200					205			
Arg	Ser	Gly	Thr	Leu	Ala	Gly	Arg	Ser	Ser	Asn	Leu				
	210					215					220				

<210> 639

<211> 1392

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1369)

<223> RXA00633

<400> 639

aaagctgcgg taattaaaaa cacttagcgc caaaaattga acactgttca attaacctat 60

tacactgcag	atatacatcc	aaaccaagtg	acggaggaaa	atg	gaa	aac	ccc	agc	115
				Met	Glu	Asn	Pro	Ser	
				1				5	

ttg	cgc	gag	ctt	gat	cac	cga	aac	atc	tgg	cac	ccg	tat	gcc	gcg	ccg	163
Leu	Arg	Glu	Leu	Asp	His	Arg	Asn	Ile	Trp	His	Pro	Tyr	Ala	Ala	Pro	
			10					15					20			

ggc	gtg	cgc	aat	aga	ctc	gtc	acc	aaa	acc	gat	gga	gtg	ttt	ttg	acg	211
Gly	Val	Arg	Asn	Arg	Leu	Val	Thr	Lys	Thr	Asp	Gly	Val	Phe	Leu	Thr	
			25					30					35			

ctg gaa gat ggc agc acc gtg att gac gcg atg agc tcc tgg tgg tcg	259
Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met Ser Ser Trp Trp Ser	
40 45 50	
gca att cat gga cac gga cac ccc cga ctg aaa gct gcc gcc caa aaa	307
Ala Ile His Gly His Gly His Pro Arg Leu Lys Ala Ala Ala Gln Lys	
55 60 65	
caa atc gac acc atg agt cac gtc atg ttt ggc gga cta acc cac gag	355
Gln Ile Asp Thr Met Ser His Val Met Phe Gly Gly Leu Thr His Glu	
70 75 80 85	
ccc gcc att aag ctc acc cac aaa ctc ctc aat ctc act gga aat tcc	403
Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn Leu Thr Gly Asn Ser	
90 95 100	
ttt gac cac gtc ttt tat tcc gat tcg ggc tcg gtc tca gtg gag gtc	451
Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser Val Ser Val Glu Val	
105 110 115	
gcc atc aaa atg gca ctg cag gcc tcc aaa gga caa ggc cac ccg gaa	499
Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly Gln Gly His Pro Glu	
120 125 130	
cgg aca aaa ctc ctc acc tgg cgg tcc ggc tac cac gga gac aca ttc	547
Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr His Gly Asp Thr Phe	
135 140 145	
acc gcg atg agc gtg tgc gac cca gaa aat ggc atg cat agc ctc tgg	595
Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly Met His Ser Leu Trp	
150 155 160 165	
aaa ggc aca ctc ccc gag cag att ttc gcc ccc gcc cca cca gtt cgg	643
Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro Ala Pro Pro Val Arg	
170 175 180	
ggg tca tcg ccg cag gcg att tcc gag tac ctg cgc agc atg gaa ttg	691
Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu Arg Ser Met Glu Leu	
185 190 195	
ctt atc gac gag gcg gtc tcc gca atc atc atc gaa ccg atc gtc caa	739
Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile Glu Pro Ile Val Gln	
200 205 210	
ggc gct gga ggc atg cgc ttt cac gat gtc gca ctc att gaa gga gtc	787
Gly Ala Gly Gly Met Arg Phe His Asp Val Ala Leu Ile Glu Gly Val	
215 220 225	
gcc aca ctg tgc aag aag cac gat cgt ttc ttg atc gtc gat gaa att	835
Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu Ile Val Asp Glu Ile	
230 235 240 245	
gcc act ggt ttc ggc cgc acc ggt gaa cta ttt gcc acg tta agc aat	883
Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe Ala Thr Leu Ser Asn	
250 255 260	
ggc cta caa cca gac atc atg tgt gtg ggc aag gcc ctc acc ggt gga	931
Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys Ala Leu Thr Gly Gly	
265 270 275	
ttc atg tcc ttc gcc gct act tta tgc acg gac aag gtg gct caa tta	979

Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp Lys Val Ala Gln Leu
 280 285 290

atc agc acc cca aat ggc gga ggt gcg ctg atg cac ggc ccc act ttt
 1027

Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met His Gly Pro Thr Phe
 295 300 305

atg gct aat cct ctg gcc tgt gcg gtt tcg cat gct tca tta gaa atc
 1075

Met Ala Asn Pro Leu Ala Cys Ala Val Ser His Ala Ser Leu Glu Ile
 310 315 320 325

att gag acc ggc atg tgg cag aaa cag gta aaa aga atc gaa gcc gaa
 1123

Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys Arg Ile Glu Ala Glu
 330 335 340

ctt atc gca ggc ctt tcc cca ctt caa cac ctt cca ggg gtt gcc gat
 1171

Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu Pro Gly Val Ala Asp
 345 350 355

gtc cgg gtt ctc ggc gcg att ggt gtc atc gaa atg gaa caa aat gtc
 1219

Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu Met Glu Gln Asn Val
 360 365 370

aat gtc gaa gaa gct act cag gct gca tta gat cac ggt gtg tgg atc
 1267

Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp His Gly Val Trp Ile
 375 380 385

cgc ccc ttt gga cgc ttg ctc tat gtc atg cct cca tat atc acc acg
 1315

Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro Pro Tyr Ile Thr Thr
 390 395 400 405

tca gag cag tgc gca cag atc tgc act gcg ctt cat gct gca gtt aaa
 1363

Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu His Ala Ala Val Lys
 410 415 420

ggg aaa taaaccatgc catttttatt tgt
 1392

Gly Lys

<210> 640

<211> 423

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 640

Met Glu Asn Pro Ser Leu Arg Glu Leu Asp His Arg Asn Ile Trp His
 1 5 10 15

Pro Tyr Ala Ala Pro Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp
 20 25 30

Gly Val Phe Leu Thr Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met
 35 40 45
 Ser Ser Trp Trp Ser Ala Ile His Gly His Gly His Pro Arg Leu Lys
 50 55 60
 Ala Ala Ala Gln Lys Gln Ile Asp Thr Met Ser His Val Met Phe Gly
 65 70 75 80
 Gly Leu Thr His Glu Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn
 85 90 95
 Leu Thr Gly Asn Ser Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser
 100 105 110
 Val Ser Val Glu Val Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly
 115 120 125
 Gln Gly His Pro Glu Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr
 130 135 140
 His Gly Asp Thr Phe Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly
 145 150 155 160
 Met His Ser Leu Trp Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro
 165 170 175
 Ala Pro Pro Val Arg Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu
 180 185 190
 Arg Ser Met Glu Leu Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile
 195 200 205
 Glu Pro Ile Val Gln Gly Ala Gly Gly Met Arg Phe His Asp Val Ala
 210 215 220
 Leu Ile Glu Gly Val Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu
 225 230 235 240
 Ile Val Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe
 245 250 255
 Ala Thr Leu Ser Asn Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys
 260 265 270
 Ala Leu Thr Gly Gly Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp
 275 280 285
 Lys Val Ala Gln Leu Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met
 290 295 300
 His Gly Pro Thr Phe Met Ala Asn Pro Leu Ala Cys Ala Val Ser His
 305 310 315 320
 Ala Ser Leu Glu Ile Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys
 325 330 335
 Arg Ile Glu Ala Glu Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu
 340 345 350
 Pro Gly Val Ala Asp Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu

	355						360						365					
Met	Glu	Gln	Asn	Val	Asn	Val	Glu	Glu	Ala	Thr	Gln	Ala	Ala	Leu	Asp			
	370					375					380							
His	Gly	Val	Trp	Ile	Arg	Pro	Phe	Gly	Arg	Leu	Leu	Tyr	Val	Met	Pro			
385					390					395					400			
Pro	Tyr	Ile	Thr	Thr	Ser	Glu	Gln	Cys	Ala	Gln	Ile	Cys	Thr	Ala	Leu			
				405					410					415				
His	Ala	Ala	Val	Lys	Gly	Lys												
	420																	
<210>	641																	
<211>	795																	
<212>	DNA																	
<213>	Corynebacterium glutamicum																	
<220>																		
<221>	CDS																	
<222>	(101)..(772)																	
<223>	RXA00632																	
<400>	641																	
tggacgcttg	ctctatgtca	tgccctccata	tatcaccacg	tcagagcagt	gcgcacagat	60												
ctgcactgcg	cttcatgctg	cagttaaagg	gaaataaac	atg	cca	ttt	tta	ttt	115									
				Met	Pro	Phe	Leu	Phe										
				1			5											
gtc	agc	ggt	acc	gga	act	ggg	gtt	ggg	aaa	acc	ttc	tcc	aca	gcc	gtt	163		
Val	Ser	Gly	Thr	Gly	Thr	Gly	Val	Gly	Lys	Thr	Phe	Ser	Thr	Ala	Val			
			10						15					20				
ttg	gtt	cga	tac	tta	gcc	gat	caa	gga	cac	gat	gtt	ctg	ccc	gta	aag	211		
Leu	Val	Arg	Tyr	Leu	Ala	Asp	Gln	Gly	His	Asp	Val	Leu	Pro	Val	Lys			
			25					30					35					
cta	gtc	caa	acc	ggt	gaa	ctt	cca	ggc	gag	gga	gac	atc	ttt	aac	att	259		
Leu	Val	Gln	Thr	Gly	Glu	Leu	Pro	Gly	Glu	Gly	Asp	Ile	Phe	Asn	Ile			
		40					45					50						
gaa	cgc	ttg	act	gga	att	gct	gga	gag	gaa	ttt	gct	cgt	ttc	aaa	gac	307		
Glu	Arg	Leu	Thr	Gly	Ile	Ala	Gly	Glu	Glu	Phe	Ala	Arg	Phe	Lys	Asp			
	55					60					65							
cct	ctt	gcg	cca	aat	ctg	gca	gcc	cga	cga	gag	ggg	gtc	gag	cca	ata	355		
Pro	Leu	Ala	Pro	Asn	Leu	Ala	Ala	Arg	Arg	Glu	Gly	Val	Glu	Pro	Ile			
	70				75					80					85			
cag	ttt	gat	cag	att	atc	tcg	tgg	ctt	cgt	ggt	ttt	gac	gac	cca	gat	403		
Gln	Phe	Asp	Gln	Ile	Ile	Ser	Trp	Leu	Arg	Gly	Phe	Asp	Asp	Pro	Asp			
			90					95						100				
cgc	atc	att	gtg	gtg	gag	ggc	gct	ggt	ggc	ctg	ctg	gtc	aga	tta	ggg	451		
Arg	Ile	Ile	Val	Val	Glu	Gly	Ala	Gly	Gly	Leu	Leu	Val	Arg	Leu	Gly			
			105					110					115					
gaa	gat	ttc	acc	ctg	qca	gat	gtt	gcc	tcc	gct	ttg	aat	qca	ccc	tta	499		

Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala Leu Asn Ala Pro Leu
 120 125 130
 gtg att gtg aca agc acc gga ttg gga agc ctc aac gct gct gaa tta 547
 Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu Asn Ala Ala Glu Leu
 135 140 145
 agc gtt gag gca gca aac cgc cga gga ctc aca gtg ttg gga gtc ctc 595
 Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr Val Leu Gly Val Leu
 150 155 160 165
 ggc ggt tcg atc cct caa aat cct gat cta gct acg atg ctt aat ctc 643
 Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala Thr Met Leu Asn Leu
 170 175 180
 gaa gaa ttt gag aga gtc acc ggc gtg ccc ttt tgg gga gct ttg ccg 691
 Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe Trp Gly Ala Leu Pro
 185 190 195
 gaa ggg ttg tca cgg gtg gag ggg ttc gtc gaa aag caa tct ttt ccg 739
 Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu Lys Gln Ser Phe Pro
 200 205 210
 gcc ctt gat gcc ttt aag aaa ccg ccg gca agg tgatcgtgaa caccgtgcct 792
 Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg
 215 220
 tcg 795

<210> 642
 <211> 224
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 642
 Met Pro Phe Leu Phe Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr
 1 5 10 15
 Phe Ser Thr Ala Val Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp
 20 25 30
 Val Leu Pro Val Lys Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly
 35 40 45
 Asp Ile Phe Asn Ile Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe
 50 55 60
 Ala Arg Phe Lys Asp Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu
 65 70 75 80
 Gly Val Glu Pro Ile Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly
 85 90 95
 Phe Asp Asp Pro Asp Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu
 100 105 110
 Leu Val Arg Leu Gly Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala
 115 120 125
 Leu Asn Ala Pro Leu Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu

130	135	140
Asn Ala Ala Glu Leu Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr		
145	150	155 160
Val Leu Gly Val Leu Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala		
	165	170 175
Thr Met Leu Asn Leu Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe		
	180	185 190
Trp Gly Ala Leu Pro Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu		
	195	200 205
Lys Gln Ser Phe Pro Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg		
210	215	220

<210> 643
 <211> 1125
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1102)
 <223> RXA00295

<400> 643
 gtttaaggca cgtgtcattt tgcattgcgcg tgcccaattc ttcttaagtg tgctcaattt 60
 ttaagcgcgc agttattgac aaccagcctc taggagatcc atg acc atc ccc ggc 115
 Met Thr Ile Pro Gly
 1 5
 acc atc ctt gac acc gcc cgc acc caa gtt ctg gaa cag gga att ggc 163
 Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu Glu Gln Gly Ile Gly
 10 15 20
 ctt aat cag cag cag ttg atg gag gtt ctc acc ttg cct gaa gag caa 211
 Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr Leu Pro Glu Glu Gln
 25 30 35
 atc cca gac ttg atg gaa tta gcc cac cag gtt cgg ttg aag tgg tgt 259
 Ile Pro Asp Leu Met Glu Leu Ala His Gln Val Arg Leu Lys Trp Cys
 40 45 50
 ggg gaa gaa atc gag gtc gag ggc att att tcc ctc aaa act ggc ggt 307
 Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser Leu Lys Thr Gly Gly
 55 60 65
 tgc cct gaa gat tgt cat ttc tgc tca cag tct ggg ttg ttt gaa tcg 355
 Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser Gly Leu Phe Glu Ser
 70 75 80 85
 ccg gtg cgt tcg gtg tgg ctg gat att ccg aat ctg gtt gaa gcc gct 403
 Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn Leu Val Glu Ala Ala
 90 95 100


```

aaa cag acc gca aaa act ggc gct acc gaa ttc tgt atc gtc gcc gca 451
Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe Cys Ile Val Ala Ala
105 110 115

gtc aag ggg cct gat gag agg ctc atg acc cag ctg gag gaa gca gtc 499
Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln Leu Glu Glu Ala Val
120 125 130

ctc gcg att cac tct gaa gtt gaa att gaa gtc gca gca tcg atc gga 547
Leu Ala Ile His Ser Glu Val Glu Ile Glu Val Ala Ala Ser Ile Gly
135 140 145

acg tta aat aag gaa cag gtg gat cgc ctc gct gct gcc ggc gtg cac 595
Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala Ala Ala Gly Val His
150 155 160 165

cgc tac aac cat aat ttg gaa act gcg cgt tcc tat ttc cct gaa gtt 643
Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser Tyr Phe Pro Glu Val
170 175 180

gtc acc act cat aca tgg gaa gag cgc cgc gaa act ttg cgc ctg gtg 691
Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu Thr Leu Arg Leu Val
185 190 195

gca gaa gct gga atg gaa gtc tgt tcc ggc gga atc tta gga atg ggc 739
Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly Ile Leu Gly Met Gly
200 205 210

gaa act tta gag cag cgc gcc gag ttt gcc gtg cag ctg gcg gag ctt 787
Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val Gln Leu Ala Glu Leu
215 220 225

gat ccg cac gaa gtc ccc atg aac ttc ctt gat cct cgc ccg ggc acc 835
Asp Pro His Glu Val Pro Met Asn Phe Leu Asp Pro Arg Pro Gly Thr
230 235 240 245

cca ttt gcc gat agg gaa ttg atg gac agc cgt gac gct ctg cgc tct 883
Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg Asp Ala Leu Arg Ser
250 255 260

att ggt gcg ttc cgc ctt gcg atg cct cac acc atg ctt cgt ttt gct 931
Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr Met Leu Arg Phe Ala
265 270 275

ggc ggt cgc gag ctg act ttg ggc gac aag ggt tcc gag caa gcc ctc 979
Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly Ser Glu Gln Ala Leu
280 285 290

ctg gga ggc atc aat gcg atg atc gtc gga aac tac ctg act acg ctc
1027
Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn Tyr Leu Thr Thr Leu
295 300 305

ggc cgc cca atg gaa gat gac ctc gac atg atg gat cgt ctc cag ctg
1075
Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met Asp Arg Leu Gln Leu
310 315 320 325

ccc atc aaa gtc ctt aat aag gtc atc taagaagcac gcgcatgaac
1122

```

Pro Ile Lys Val Leu Asn Lys Val Ile
330

gac
1125

<210> 644

<211> 334

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 644

Met	Thr	Ile	Pro	Gly	Thr	Ile	Leu	Asp	Thr	Ala	Arg	Thr	Gln	Val	Leu	1	5	10	15
Glu	Gln	Gly	Ile	Gly	Leu	Asn	Gln	Gln	Gln	Leu	Met	Glu	Val	Leu	Thr	20	25	30	
Leu	Pro	Glu	Glu	Gln	Ile	Pro	Asp	Leu	Met	Glu	Leu	Ala	His	Gln	Val	35	40	45	
Arg	Leu	Lys	Trp	Cys	Gly	Glu	Glu	Ile	Glu	Val	Glu	Gly	Ile	Ile	Ser	50	55	60	
Leu	Lys	Thr	Gly	Gly	Cys	Pro	Glu	Asp	Cys	His	Phe	Cys	Ser	Gln	Ser	65	70	75	80
Gly	Leu	Phe	Glu	Ser	Pro	Val	Arg	Ser	Val	Trp	Leu	Asp	Ile	Pro	Asn	85	90	95	
Leu	Val	Glu	Ala	Ala	Lys	Gln	Thr	Ala	Lys	Thr	Gly	Ala	Thr	Glu	Phe	100	105	110	
Cys	Ile	Val	Ala	Ala	Val	Lys	Gly	Pro	Asp	Glu	Arg	Leu	Met	Thr	Gln	115	120	125	
Leu	Glu	Glu	Ala	Val	Leu	Ala	Ile	His	Ser	Glu	Val	Glu	Ile	Glu	Val	130	135	140	
Ala	Ala	Ser	Ile	Gly	Thr	Leu	Asn	Lys	Glu	Gln	Val	Asp	Arg	Leu	Ala	145	150	155	160
Ala	Ala	Gly	Val	His	Arg	Tyr	Asn	His	Asn	Leu	Glu	Thr	Ala	Arg	Ser	165	170	175	
Tyr	Phe	Pro	Glu	Val	Val	Thr	Thr	His	Thr	Trp	Glu	Glu	Arg	Arg	Glu	180	185	190	
Thr	Leu	Arg	Leu	Val	Ala	Glu	Ala	Gly	Met	Glu	Val	Cys	Ser	Gly	Gly	195	200	205	
Ile	Leu	Gly	Met	Gly	Glu	Thr	Leu	Glu	Gln	Arg	Ala	Glu	Phe	Ala	Val	210	215	220	
Gln	Leu	Ala	Glu	Leu	Asp	Pro	His	Glu	Val	Pro	Met	Asn	Phe	Leu	Asp	225	230	235	240
Pro	Arg	Pro	Gly	Thr	Pro	Phe	Ala	Asp	Arg	Glu	Leu	Met	Asp	Ser	Arg	245	250	255	

Asp Ala Leu Arg Ser Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr
 260 265 270

Met Leu Arg Phe Ala Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly
 275 280 285

Ser Glu Gln Ala Leu Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn
 290 295 300

Tyr Leu Thr Thr Leu Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met
 305 310 315 320

Asp Arg Leu Gln Leu Pro Ile Lys Val Leu Asn Lys Val Ile
 325 330

<210> 645

<211> 1212

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1189)

<223> RXA00223

<400> 645

gcgacctctt tgacatcgcc cctgcgctca tcgaagagat caacaagcgc aagtaggagt 60

tttgaacact ttttatctgg accatgcagc caccacacca atg cgt gag gtg gcc 115
 Met Arg Glu Val Ala
 1 5

gca gct gcg tgg atg gaa aac gcg cag gca ttg aat ccc gcg agt cag 163
 Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu Asn Pro Ala Ser Gln
 10 15 20

tac ggt tcg ggg cgt aag gcg cgc agc gtt gcg gat tcg gct cgt gaa 211
 Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala Asp Ser Ala Arg Glu
 25 30 35

gaa att gct tct ttg ctg ggc tgt gaa cct atc gag gtt gtg ttt acc 259
 Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile Glu Val Val Phe Thr
 40 45 50

gcg tcc ggc acg gag gca gat aac ctc gct gtg cag ggg tta ttc cac 307
 Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val Gln Gly Leu Phe His
 55 60 65

gca tcg cct ctc aat cgg att att tct acg ccg atc gag cac ccc ggg 355
 Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro Ile Glu His Pro Gly
 70 75 80 85

att ctg gaa acc gtc aag gct cta gaa ctt ggc ggg gca gag gcg gag 403
 Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly Gly Ala Glu Ala Glu
 90 95 100

ctc atg ccg atc ggt cca gat gga cga gtg tct tcc ttc gaa gcg ctg 451
 Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser Ser Phe Glu Ala Leu
 105 110 115

gac aag cct gcc gcg gtt gcc act atg atg tgg gcg aac aat gag acc 499
 Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp Ala Asn Asn Glu Thr
 120 125 130

ggc gcg att cag ccg gtt tct gag ttc atc gcc gcc gcg cag gcg tcc 547
 Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala Ala Ala Gln Ala Ser
 135 140 145

ggc acg cca aca cac atc gat gcg gtt cag gtc gtt ggc cat ctg ccg 595
 Gly Thr Pro Thr His Ile Asp Ala Val Gln Val Val Gly His Leu Pro
 150 155 160 165

gtc aat ttt gat gag ctc ggc gcc acc act ttg gct gcc tcc gcg cac 643
 Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu Ala Ala Ser Ala His
 170 175 180

aaa ttc ggt gga cca cgt ggc gtc ggc ctg ctg ttg gtg agg cgc tca 691
 Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu Leu Val Arg Arg Ser
 185 190 195

cca gca cct tca gcc gta ttg cac gga ggt ggt cag gag cgc ggc atc 739
 Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly Gln Glu Arg Gly Ile
 200 205 210

cgt cca ggc acc ctt gat gtc gcc ggc gca gct gcc acc gca gcc gca 787
 Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala Ala Thr Ala Ala Ala
 215 220 225

tta cgc gaa gca gtg gcc gag ctt gac ggc gaa gcc acc cgc ctg cgc 835
 Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu Ala Thr Arg Leu Arg
 230 235 240 245

gga ctt aaa aag atg ctt ctc gac gcc atc ctc cac acc atc ccc aac 883
 Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu His Thr Ile Pro Asn
 250 255 260

gta ctg gtc cac acc acc gaa cca tcc ctg cca gga cac ctg cat ctc 931
 Val Leu Val His Thr Thr Glu Pro Ser Leu Pro Gly His Leu His Leu
 265 270 275

tcc ttc cca gga gca gaa ggc gat agt ttg atc atg ctg ctc gac tcc 979
 Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile Met Leu Leu Asp Ser
 280 285 290

ttg cgg atc gaa gcc tcc aca ggt tcg gcc tgc tcc aac ggt gta aac
 1027
 Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys Ser Asn Gly Val Asn
 295 300 305

cgt gcc agc cac gtc ctt ttg gcc atg gga att tcc gaa acc gac gcc
 1075
 Arg Ala Ser His Val Leu Leu Ala Met Gly Ile Ser Glu Thr Asp Ala
 310 315 320 325

cgt ggt gcc atc cga ttc acc ctc gga aga acc acc act gaa gaa tcc
 1123
 Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr Thr Thr Glu Glu Ser
 330 335 340

atc aag gca gtg atc gcc gtg atc gaa gac gta gtg acc agg gct cgt
 1171

Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val Val Thr Arg Ala Arg
 345 350 355

act gcg gga atg gct ttt tagcgaccgt aaatcgcata gtg
 1212

Thr Ala Gly Met Ala Phe
 360

<210> 646

<211> 363

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 646

Met Arg Glu Val Ala Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu
 1 5 10 15

Asn Pro Ala Ser Gln Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala
 20 25 30

Asp Ser Ala Arg Glu Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile
 35 40 45

Glu Val Val Phe Thr Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val
 50 55 60

Gln Gly Leu Phe His Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro
 65 70 75 80

Ile Glu His Pro Gly Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly
 85 90 95

Gly Ala Glu Ala Glu Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser
 100 105 110

Ser Phe Glu Ala Leu Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp
 115 120 125

Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala
 130 135 140

Ala Ala Gln Ala Ser Gly Thr Pro Thr His Ile Asp Ala Val Gln Val
 145 150 155 160

Val Gly His Leu Pro Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu
 165 170 175

Ala Ala Ser Ala His Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu
 180 185 190

Leu Val Arg Arg Ser Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly
 195 200 205

Gln Glu Arg Gly Ile Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala
 210 215 220

Ala Thr Ala Ala Ala Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu
 225 230 235 240

Ala Thr Arg Leu Arg Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu

				245						250						255			
His	Thr	Ile	Pro	Asn	Val	Leu	Val	His	Thr	Thr	Glu	Pro	Ser	Leu	Pro				
			260					265						270					
Gly	His	Leu	His	Leu	Ser	Phe	Pro	Gly	Ala	Glu	Gly	Asp	Ser	Leu	Ile				
		275					280					285							
Met	Leu	Leu	Asp	Ser	Leu	Arg	Ile	Glu	Ala	Ser	Thr	Gly	Ser	Ala	Cys				
	290					295						300							
Ser	Asn	Gly	Val	Asn	Arg	Ala	Ser	His	Val	Leu	Leu	Ala	Met	Gly	Ile				
305					310					315					320				
Ser	Glu	Thr	Asp	Ala	Arg	Gly	Ala	Ile	Arg	Phe	Thr	Leu	Gly	Arg	Thr				
				325					330					335					
Thr	Thr	Glu	Glu	Ser	Ile	Lys	Ala	Val	Ile	Ala	Val	Ile	Glu	Asp	Val				
			340					345					350						
Val	Thr	Arg	Ala	Arg	Thr	Ala	Gly	Met	Ala	Phe									
		355					360												
<210>	647																		
<211>	1197																		
<212>	DNA																		
<213>	Corynebacterium glutamicum																		
<220>																			
<221>	CDS																		
<222>	(101)..(1174)																		
<223>	RXN00262																		
<400>	647																		
acaccgcggg	aaagattgca	tcaaccggtg	tcgacgtcat	ttccgttgga	gcgcttaccc	60													
attctgtgca	tgcacttgac	ctaggactcg	atattttcta	atg ctc tac ctt gat	115														
				Met Leu Tyr Leu Asp															
				1	5														
aat gca gcc acc acc agt gtg cgc aat gaa gca ctt gag gcc atg tgg	163																		
Asn Ala Ala Thr	10																		
cct tat ctc acc gga gcg ttt ggc aat ccg tca agt ccc cat gag gtg	211																		
Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser Ser Pro His Glu Val																			
	25							30						35					
gga aga ctc gcc tct gcg ggg ctg gag gat gct cga act cgg gtg gcc	259																		
Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala Arg Thr Arg Val Ala																			
	40						45						50						
cgc att atc gga gga cgc ccc aca cag gtg acg ttt acg tcg ggt gga	307																		
Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr P																			

cgt ggc cgg cac ctc atc acc acc ccg atc gag cat gac agt gtc cta	403
Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu	
90 95 100	
gaa act gct gct tat ctt gaa agg ttt cat gat ttc gag atc acc tac	451
Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr	
105 110 115	
cta tcc ccc gat cac act ggg ctg atc tcc ccg gag ggt ctc cgc aaa	499
Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys	
120 125 130	
gca gtc agg ccg gac acc aca ttg atc agc att ggt tat gcc aac aat	547
Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn	
135 140 145	
gag gtg gga acc att cag ccg ata gct gag ttg gcg gcg gta agc agt	595
Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser	
150 155 160 165	
acg cct ttt cac acc gat gca gtg caa gct gca cat tta acc ttt gac	643
Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp	
170 175 180	
ttg gga gtt gac gcg tta agt ttg tcg ggt cat aaa ttc ggt gcg cct	691
Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro	
185 190 195	
aaa ggg att gga gtg tta tgg tca aag ctt ccc ctg gag ccg gta atc	739
Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile	
200 205 210	
cat ggc ggc ggc cag gaa aaa ggg ccg cgt agt ggc acg gaa aac gtt	787
His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val	
215 220 225	
gcg ggg gct atc gcc ttt gcc act gcc ttg gaa ttg gcc agg gcg gaa	835
Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu	
230 235 240 245	
tcc tat cca gat ctt ggc gaa ttc atc gag gaa gtt ctc act atc ccg	883
Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro	
250 255 260	
gga gca cac ctg act gga cat cct agg atg cgc att gat gga cac gca	931
Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala	
265 270 275	
tct ttt ctc ttc gac agc ata gga tct gaa act gtt ctt ctg gaa ttg	979
Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu	
280 285 290	
gaa cgc caa ggc att gtg tgc tcc cct ggt tct gcc tgt ggt tcc gga	
1027	
Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly	
295 300 305	
gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt gag gag gat caa gca	
1075	
Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala	
310 315 320 325	

cga acg gct gtg cgc tgt act ttt agt aca aca cac agc cgt gaa gat
1123

Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp
330 335 340

gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg gtc gcc tta atc aga
1171

Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg
345 350 355

ggg tgacgctagt cagaggttta cgg

1197

Gly

<210> 648

<211> 358

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 648

Met Leu Tyr Leu Asp Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala
1 5 10 15

Leu Glu Ala Met Trp Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser
20 25 30

Ser Pro His Glu Val Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala
35 40 45

Arg Thr Arg Val Ala Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr
50 55 60

Phe Thr Ser Gly Gly Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala
65 70 75 80

Cys Leu Ala Asn Pro Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu
85 90 95

His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp
100 105 110

Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro
115 120 125

Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile
130 135 140

Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
145 150 155 160

Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
165 170 175

His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
180 185 190

Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
195 200 205

Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
 210 215 220
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
 225 230 235 240
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
 245 250 255
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
 260 265 270
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
 275 280 285
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
 290 295 300
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
 305 310 315 320
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
 325 330 335
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
 340 345 350
 Val Ala Leu Ile Arg Gly
 355

<210> 649
 <211> 920
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (79)..(897)
 <223> FRXA00262

<400> 649
 cacacaggtg acgtttacgt cgggtggatc agaagccaac aacctcgctt atcaaaggag 60
 cgtgcttagc taatcctagtg gcc ggg cac ctc atc acc acc ccg atc gag 111
 Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu
 1 5 10
 cat gac agt gtc cta gaa act gct gct tat ctt gaa agg ttt cat gat 159
 His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp
 15 20 25
 ttc gag atc acc tac cta tcc ccc gat cac act ggg ctg atc tcc ccg 207
 Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro
 30 35 40
 gag ggt ctc cgc aaa gca gtc agg ccg gac acc aca ttg atc agc att 255
 Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile
 45 50 55

ggt tat gcc aac aat gag gtg gga acc att cag ccg ata gct gag ttg 303
 Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
 60 65 70 75
 gcg gcg gta agc agt acg cct ttt cac acc gat gca gtg caa gct gca 351
 Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
 80 85 90
 cat tta acc ttt gac ttg gga gtt gac gcg tta agt ttg tcg ggt cat 399
 His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
 95 100 105
 aaa ttc ggt gcg cct aaa ggg att gga gtg tta tgg tca aag ctt ccc 447
 Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
 110 115 120
 ctg gag ccg gta atc cat ggc ggc ggc cag gaa aaa ggg cgg cgt agt 495
 Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
 125 130 135
 ggc acg gaa aac gtt gcg ggg gct atc gcc ttt gcc act gcc ttg gaa 543
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
 140 145 150 155
 ttg gcc agg gcg gaa tcc tat cca gat ctt ggc gaa ttc atc gag gaa 591
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
 160 165 170
 gtt ctc act atc ccg gga gca cac ctg act gga cat cct agg atg cgc 639
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
 175 180 185
 att gat gga cac gca tct ttt ctc ttc gac agc ata gga tct gaa act 687
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
 190 195 200
 gtt ctt ctg gaa ttg gaa cgc caa ggc att gtg tgc tcc cct ggt tct 735
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
 205 210 215
 gcc tgt ggt tcc gga gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt 783
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
 220 225 230 235
 gag gag gat caa gca cga acg gct gtg cgc tgt act ttt agt aca aca 831
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
 240 245 250
 cac agc cgt gaa gat gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg 879
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
 255 260 265
 gtc gcc tta atc aga ggg tgacgctagt cagaggttta cgg 920
 Val Ala Leu Ile Arg Gly
 270

<210> 650

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 650

Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu
 1 5 10 15
 Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr
 20 25 30
 Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys
 35 40 45
 Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn
 50 55 60
 Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser
 65 70 75 80
 Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp
 85 90 95
 Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro
 100 105 110
 Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile
 115 120 125
 His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val
 130 135 140
 Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu
 145 150 155 160
 Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro
 165 170 175
 Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala
 180 185 190
 Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu
 195 200 205
 Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly
 210 215 220
 Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala
 225 230 235 240
 Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp
 245 250 255
 Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg
 260 265 270

Gly

<210> 651

<211> 1296

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1273)

<223> RXN00435

<400> 651

cgacaggtga attcatgcac gtttgagtgt cccgtgtgtg gggtaatggt gtccaagaga 60

gtggaaggaa atgctgtggc ggttgaaagg agtgcctttc gtg ggt ttt gat gtg 115
Val Gly Phe Asp Val
1 5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr
10 15 20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly
25 30 35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser
40 45 50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala
55 60 65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg
70 75 80 85

cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403
Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg
90 95 100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr
105 110 115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp
120 125 130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac gag aag ctt gtt gac 547
Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Glu Lys Leu Val Asp
135 140 145

ggc tcg acg cgc ctt gtc gtg ctc agc gcc gcg cac ccg ctg ctc ggc 595
Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala His Pro Leu Leu Gly
150 155 160 165

acg gtc gcc cca gtg ggc aag att gtg gat aaa gtg cgg gcg cgt tcg 643
Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys Val Arg Ala Arg Ser
170 175 180

cgt gcc tgg gtg ctt gtc gac gcc acc acc tac gca gcc tac cgc ccc 691
Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro
185 190 195

ctg cgc cta gac gag tgg gaa gcc gat atc gtc atg ctt gat ctc ggc 739
 Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly
 200 205 210

gag ttg ggc ggc ccg cag att tcg gcg ttg att ttc cgt gat acc tcg 787
 Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser
 215 220 225

atg ttc ccg cgc ctg gat cgc acc gtt cca ctc gaa ctg ccc gca agc 835
 Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser
 230 235 240 245

tcc ctg ccg cat ggg ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac 883
 Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro Asn Leu Val Arg His
 250 255 260

ctg gga aac ctg gat gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg 931
 Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly
 265 270 275

gag atg gcg aaa ttc cac aag gga ctt ttt gag cat ctt gtg gaa tcg 979
 Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu His Leu Val Glu Ser
 280 285 290

ctc gaa gga ctt cac gcg gtg cat atc gtg gga att tcc ggc gat gcc
 1027
 Leu Glu Gly Leu His Ala Val His Ile Val Gly Ile Ser Gly Asp Ala
 295 300 305

gca ggt caa gac gcc ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc
 1075
 Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe
 310 315 320 325

acc atg gaa ggc gtg ccc gca gat atg gtg tac cgc cga ttg gtg gac
 1123
 Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp
 330 335 340

aat cgt ttg atc act acc gtc agc cct gct gac ccg ctg ctc gaa gca
 1171
 Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala
 345 350 355

atg ggt gtg act gaa gct ggc gga tcg atc act atc gga cta agc ccg
 1219
 Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro
 360 365 370

ttt agc acc tac tat gaa gtg gat cag ctg acc agg gtg ctg gca tcg
 1267
 Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser
 375 380 385

ctt gcc taaaccgcaa gcacgagctt gcc
 1296
 Leu Ala
 390

<210> 652

<211> 391

<212> PRT

<213> Corynebacterium glutamicum

<400> 652

Val	Gly	Phe	Asp	Val	Ala	Arg	Val	Arg	Gly	Leu	Tyr	Thr	Ser	Leu	Gly	1	5	10	15
Asp	Gly	Trp	Thr	Tyr	Leu	Asn	Ser	His	Gln	Ile	Pro	Gln	Val	Pro	Glu	20	25	30	
Arg	Val	Ala	Ser	Gly	Val	Ala	Ala	Ala	Phe	Arg	Thr	His	Ala	Gln	Ile	35	40	45	
Ser	Glu	Val	Thr	Ser	Gln	Pro	Ile	Ala	Val	Asp	Gln	Leu	Glu	Ala	Ala	50	55	60	
Arg	Glu	Ala	Val	Ala	Ser	Leu	Ala	Gly	Val	Asp	Pro	Asp	Cys	Val	Val	65	70	75	80
Leu	Gly	Pro	Thr	Arg	Gln	Phe	Leu	Ala	His	Thr	Leu	Ala	Arg	Gly	Leu	85	90	95	
Gly	Gly	Phe	Val	Arg	Arg	Lys	Ala	Gly	Val	Val	Leu	Ser	Arg	Ala	Asp	100	105	110	
Ala	Asp	Trp	Leu	Thr	Ala	Pro	Phe	Arg	Ser	Leu	Asp	Gly	Val	Phe	Ser	115	120	125	
Trp	Ala	Glu	Pro	Asp	Leu	Gly	Thr	Gly	Met	Leu	Pro	Asp	Trp	Gln	Tyr	130	135	140	
Glu	Lys	Leu	Val	Asp	Gly	Ser	Thr	Arg	Leu	Val	Val	Leu	Ser	Ala	Ala	145	150	155	160
His	Pro	Leu	Leu	Gly	Thr	Val	Ala	Pro	Val	Gly	Lys	Ile	Val	Asp	Lys	165	170	175	
Val	Arg	Ala	Arg	Ser	Arg	Ala	Trp	Val	Leu	Val	Asp	Ala	Thr	Thr	Tyr	180	185	190	
Ala	Ala	Tyr	Arg	Pro	Leu	Arg	Leu	Asp	Glu	Trp	Glu	Ala	Asp	Ile	Val	195	200	205	
Met	Leu	Asp	Leu	Gly	Glu	Leu	Gly	Gly	Pro	Gln	Ile	Ser	Ala	Leu	Ile	210	215	220	
Phe	Arg	Asp	Thr	Ser	Met	Phe	Pro	Arg	Leu	Asp	Arg	Thr	Val	Pro	Leu	225	230	235	240
Glu	Leu	Pro	Ala	Ser	Ser	Leu	Pro	His	Gly	Leu	Leu	Gly	Gly	Val	Pro	245	250	255	
Asn	Leu	Val	Arg	His	Leu	Gly	Asn	Leu	Asp	Glu	Asn	Ala	Pro	Ser	Val	260	265	270	
Val	Glu	Ala	Met	Gly	Glu	Met	Ala	Lys	Phe	His	Lys	Gly	Leu	Phe	Glu	275	280	285	
His	Leu	Val	Glu	Ser	Leu	Glu	Gly	Leu	His	Ala	Val	His	Ile	Val	Gly	290	295	300	

Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val
 305 310 315 320

Pro Arg Leu Thr Phe Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr
 325 330 335

Arg Arg Leu Val Asp Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp
 340 345 350

Pro Leu Leu Glu Ala Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr
 355 360 365

Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr
 370 375 380

Arg Val Leu Ala Ser Leu Ala
 385 390

<210> 653

<211> 638

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(615)

<223> FRXA00435

<400> 653

gtc gac gcc acc acc tac gca gcc tac cgc ccc ctg cgc cta gac gag	48
Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu	
1 5 10 15	
tg gaa gcc gat atc gtc atg ctt gat ctc ggc gag ttg ggc ggc ccg	96
Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro	
20 25 30	
cag att tcg gcg ttg att ttc cgt gat acc tcg atg ttc ccg cgc ctg	144
Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu	
35 40 45	
gat cgc acc gtt cca ctc gaa ctg ccc gca agc tcc ctg ccg cat ggg	192
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly	
50 55 60	
ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac ctg gga aac ctg gat	240
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp	
65 70 75 80	
gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg gag atg gcg aaa ttc	288
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe	
85 90 95	
cac aag gga ctt ttt gag cat ctt gtg gaa tcg ctc gaa gga ctt cac	336
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His	
100 105 110	
gcg gtg cat atc gtg gga att tcc ggc gat gcc gca ggt caa gac gcc	384
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala	

115	120	125	
ccg ttc ctg gat cga gtg	ccc cgc ttg acc ttc acc	atg gaa ggc gtg	432
Pro Phe Leu Asp Arg Val	Pro Arg Leu Thr Phe Thr	Met Glu Gly Val	
130	135	140	
ccc gca gat atg gtg tac	cgc cga ttg gtg gac aat	cgt ttg atc act	480
Pro Ala Asp Met Val Tyr	Arg Arg Leu Val Asp Asn	Arg Leu Ile Thr	
145	150	155	160
acc gtc agc cct gct gac	ccg ctg ctc gaa gca atg	ggg gtg act gaa	528
Thr Val Ser Pro Ala Asp	Pro Leu Leu Glu Ala Met	Gly Val Thr Glu	
165	170	175	
gct ggc gga tcg atc act	atc gga cta agc ccg ttt	agc acc tac tat	576
Ala Gly Gly Ser Ile Thr	Ile Gly Leu Ser Pro Phe	Ser Thr Tyr Tyr	
180	185	190	
gaa gtg gat cag ctg acc	agg gtg ctg gca tcg ctt	gcc taaaccgcaa	625
Glu Val Asp Gln Leu Thr	Arg Val Leu Ala Ser Leu	Ala	
195	200	205	
gcacgagctt gcc			638

<210> 654

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 654

Val Asp Ala Thr Thr Tyr	Ala Ala Tyr Arg Pro	Leu Arg Leu Asp Glu
1	5	10
15		

Trp Glu Ala Asp Ile Val	Met Leu Asp Leu Gly	Glu Leu Gly Gly Pro
20	25	30

Gln Ile Ser Ala Leu Ile	Phe Arg Asp Thr Ser	Met Phe Pro Arg Leu
35	40	45

Asp Arg Thr Val Pro Leu	Glu Leu Pro Ala Ser	Ser Leu Pro His Gly
50	55	60

Leu Leu Gly Gly Val Pro	Asn Leu Val Arg His	Leu Gly Asn Leu Asp
65	70	75
80		

Glu Asn Ala Pro Ser Val	Val Glu Ala Met Gly	Glu Met Ala Lys Phe
85	90	95

His Lys Gly Leu Phe Glu	His Leu Val Glu Ser	Leu Glu Gly Leu His
100	105	110

Ala Val His Ile Val Gly	Ile Ser Gly Asp Ala	Ala Gly Gln Asp Ala
115	120	125

Pro Phe Leu Asp Arg Val	Pro Arg Leu Thr Phe	Thr Met Glu Gly Val
130	135	140

Pro Ala Asp Met Val Tyr	Arg Arg Leu Val Asp	Asn Arg Leu Ile Thr
145	150	155
		160

Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala Met Gly Val Thr Glu
165 170 175

Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr
180 185 190

Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala
195 200 205

<210> 655

<211> 535

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA02801

<400> 655

cgacaggtga attcatgcac gtttgagtgt cccgtgtgtg gggtaatggt gtccaagaga 60

gtggaaggaa atgctgtggc gggtgaaagg agtgcctttc gtg ggt ttt gat gtg 115
Val Gly Phe Asp Val
1 5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr
10 15 20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly
25 30 35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser
40 45 50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala
55 60 65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg
70 75 80 85

cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403
Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg
90 95 100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr
105 110 115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp
120 125 130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac cag 535
Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Gln

```

135                                140                                145

<210> 656
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 656
Val Gly Phe Asp Val Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly
  1                                5                                10                                15

Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu
      20                                25                                30

Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile
      35                                40                                45

Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
  50                                55                                60

Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
  65                                70                                75                                80

Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
      85                                90                                95

Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
      100                                105                                110

Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
      115                                120                                125

Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
      130                                135                                140

Gln
145

```

```
<210> 657
<211> 1386
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1363)
<223> RXA02516
```

```

<400> 657
ttcattcacg ttttcgcgaa tggccagatt gtgaccaccg gtggcgctga gcttgctgac 60
aagctcgagg ctgacggcta cgaccagttc atcaagtaac atg tcc gat ttc ctc      115
                                         Met Ser Asp Phe Leu
                                         1                               5

aat gca gat gga tcc ctc aat gtg gat aag gtg cgg gaa gaa ttc cca      163
Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val Arg Glu Glu Phe Pro
                        10                        15                        20

```

atc ctg aag cgc act gtt agg gat ggg aaa ccg ctt gct tac ctg gac	211
Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro Leu Ala Tyr Leu Asp	
25 30 35	
tca ggt gcg aca tcg cag cga ccc gag cgg gtg tgg cgt gca gag gag	259
Ser Gly Ala Thr Ser Gln Arg Pro Glu Arg Val Trp Arg Ala Glu Glu	
40 45 50	
cac ttt gtg ctg cac acc aac gcc ccc gtg cac cgc ggt gcc tac caa	307
His Phe Val Leu His Thr Asn Ala Pro Val His Arg Gly Ala Tyr Gln	
55 60 65	
ctg gct gag gaa gca acg gat gct tat gaa ggt gcc cgc gag aag atc	355
Leu Ala Glu Glu Ala Thr Asp Ala Tyr Glu Gly Ala Arg Glu Lys Ile	
70 75 80 85	
gct gcc ttt gtt ggt gcc gag cag cat gaa att gcg ttc act aag aat	403
Ala Ala Phe Val Gly Ala Glu Gln His Glu Ile Ala Phe Thr Lys Asn	
90 95 100	
gca act gaa gca ctc aat ctt gtt gcg tac acc ttg ggt gat gac cgt	451
Ala Thr Glu Ala Leu Asn Leu Val Ala Tyr Thr Leu Gly Asp Asp Arg	
105 110 115	
tcc ggt aag tat cgt gtc cag gcc ggg gat acc gtg gtc atc acg gag	499
Ser Gly Lys Tyr Arg Val Gln Ala Gly Asp Thr Val Val Ile Thr Glu	
120 125 130	
cta gag cac cac gca aac ttg gtg cca tgg cag gag ctg tgc cgt cga	547
Leu Glu His His Ala Asn Leu Val Pro Trp Gln Glu Leu Cys Arg Arg	
135 140 145	
acc ggt gcg aca ttg aag tgg tac aag gtg act gaa gat ggt cgc att	595
Thr Gly Ala Thr Leu Lys Trp Tyr Lys Val Thr Glu Asp Gly Arg Ile	
150 155 160 165	
gat ctc gat tca ctc gag ctt gat gaa act gtc aag gtc gtt gcc ttc	643
Asp Leu Asp Ser Leu Glu Leu Asp Glu Thr Val Lys Val Val Ala Phe	
170 175 180	
act cac cag tcc aat gtg acc ggt gct gtg gct gat gtt cca gag ttg	691
Thr His Gln Ser Asn Val Thr Gly Ala Val Ala Asp Val Pro Glu Leu	
185 190 195	
gtt cgt cgt gcc aag gct gtc ggc gct ctc acg gtg ctt gat gcg tgc	739
Val Arg Arg Ala Lys Ala Val Gly Ala Leu Thr Val Leu Asp Ala Cys	
200 205 210	
cag tct gtt cct cat atg cca gtg aat ttc cac gag ctg gat gta gat	787
Gln Ser Val Pro His Met Pro Val Asn Phe His Glu Leu Asp Val Asp	
215 220 225	
ttc tct gca ttc tct ggc cat aag atg ctg gga cct gca ggc gtg ggc	835
Phe Ser Ala Phe Ser Gly His Lys Met Leu Gly Pro Ala Gly Val Gly	
230 235 240 245	
gtt gtg tat gca aag tcc cca atc ttg gat gaa ctg cca cca ttt ttg	883
Val Val Tyr Ala Lys Ser Pro Ile Leu Asp Glu Leu Pro Pro Phe Leu	
250 255 260	
act ggt ggt tcc atg att gaa gtt gtc acc atg gag ggt tcc acc tac	931

Thr Gly Gly Ser Met Ile Glu Val Val Thr Met Glu Gly Ser Thr Tyr
 265 270 275
 gct gcc gca cct caa cgt ttt gag gcc ggc acg cag atg acc agc cag 979
 Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr Gln Met Thr Ser Gln
 280 285 290
 gtt gtg ggc ttg ggt gct gcc gtg gac atg ctg aat gaa atc ggt atg
 1027
 Val Val Gly Leu Gly Ala Ala Val Asp Met Leu Asn Glu Ile Gly Met
 295 300 305
 gaa gca atc gca gcg cat gag cac gca ttg act gct tac gcg ttg gaa
 1075
 Glu Ala Ile Ala Ala His Glu His Ala Leu Thr Ala Tyr Ala Leu Glu
 310 315 320 325
 aag ctc acg gca att aag gga cta acc att gct ggt cct ttg act gca
 1123
 Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala Gly Pro Leu Thr Ala
 330 335 340
 gag cag cgc ggc ggt gca atc agc ttc ggt gtc gag ggc att cac cca
 1171
 Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val Glu Gly Ile His Pro
 345 350 355
 cac gat cta ggc caa gtg ctt gac gat cag ggc gtg aat atc cgc gtc
 1219
 His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly Val Asn Ile Arg Val
 360 365 370
 ggc cac cac tgc gcg tgg ccc gtg cac cgc agc atg aac gta caa tcg
 1267
 Gly His His Cys Ala Trp Pro Val His Arg Ser Met Asn Val Gln Ser
 375 380 385
 aca gca aga gca tct ttc tat ctc tat aac acc ttc gaa gaa atc gac
 1315
 Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr Phe Glu Glu Ile Asp
 390 395 400 405
 cgc ctc gcg gca gcg atc gag aag gcc aag caa ttc ttt gga gtt gag
 1363
 Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln Phe Phe Gly Val Glu
 410 415 420
 taatgaacct tgagcagatg tac
 1386

<210> 658

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 658

Met Ser Asp Phe Leu Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val
 1 5 10 15

Arg Glu Glu Phe Pro Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro

20					25					30					
Leu	Ala	Tyr	Leu	Asp	Ser	Gly	Ala	Thr	Ser	Gln	Arg	Pro	Glu	Arg	Val
	35						40					45			
Trp	Arg	Ala	Glu	Glu	His	Phe	Val	Leu	His	Thr	Asn	Ala	Pro	Val	His
	50					55					60				
Arg	Gly	Ala	Tyr	Gln	Leu	Ala	Glu	Glu	Ala	Thr	Asp	Ala	Tyr	Glu	Gly
	65					70					75				80
Ala	Arg	Glu	Lys	Ile	Ala	Ala	Phe	Val	Gly	Ala	Glu	Gln	His	Glu	Ile
				85					90					95	
Ala	Phe	Thr	Lys	Asn	Ala	Thr	Glu	Ala	Leu	Asn	Leu	Val	Ala	Tyr	Thr
			100					105						110	
Leu	Gly	Asp	Asp	Arg	Ser	Gly	Lys	Tyr	Arg	Val	Gln	Ala	Gly	Asp	Thr
		115					120					125			
Val	Val	Ile	Thr	Glu	Leu	Glu	His	His	Ala	Asn	Leu	Val	Pro	Trp	Gln
	130					135					140				
Glu	Leu	Cys	Arg	Arg	Thr	Gly	Ala	Thr	Leu	Lys	Trp	Tyr	Lys	Val	Thr
	145					150					155				160
Glu	Asp	Gly	Arg	Ile	Asp	Leu	Asp	Ser	Leu	Glu	Leu	Asp	Glu	Thr	Val
				165					170					175	
Lys	Val	Val	Ala	Phe	Thr	His	Gln	Ser	Asn	Val	Thr	Gly	Ala	Val	Ala
			180					185					190		
Asp	Val	Pro	Glu	Leu	Val	Arg	Arg	Ala	Lys	Ala	Val	Gly	Ala	Leu	Thr
		195					200					205			
Val	Leu	Asp	Ala	Cys	Gln	Ser	Val	Pro	His	Met	Pro	Val	Asn	Phe	His
	210					215					220				
Glu	Leu	Asp	Val	Asp	Phe	Ser	Ala	Phe	Ser	Gly	His	Lys	Met	Leu	Gly
	225					230					235				240
Pro	Ala	Gly	Val	Gly	Val	Val	Tyr	Ala	Lys	Ser	Pro	Ile	Leu	Asp	Glu
				245					250					255	
Leu	Pro	Pro	Phe	Leu	Thr	Gly	Gly	Ser	Met	Ile	Glu	Val	Val	Thr	Met
			260					265						270	
Glu	Gly	Ser	Thr	Tyr	Ala	Ala	Ala	Pro	Gln	Arg	Phe	Glu	Ala	Gly	Thr
		275					280					285			
Gln	Met	Thr	Ser	Gln	Val	Val	Gly	Leu	Gly	Ala	Ala	Val	Asp	Met	Leu
	290					295					300				
Asn	Glu	Ile	Gly	Met	Glu	Ala	Ile	Ala	Ala	His	Glu	His	Ala	Leu	Thr
	305					310					315				320
Ala	Tyr	Ala	Leu	Glu	Lys	Leu	Thr	Ala	Ile	Lys	Gly	Leu	Thr	Ile	Ala
				325					330					335	
Gly	Pro	Leu	Thr	Ala	Glu	Gln	Arg	Gly	Gly	Ala	Ile	Ser	Phe	Gly	Val
			340					345					350		

Glu Gly Ile His Pro His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly
 355 360 365
 Val Asn Ile Arg Val Gly His His Cys Ala Trp Pro Val His Arg Ser
 370 375 380
 Met Asn Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr
 385 390 395 400
 Phe Glu Glu Ile Asp Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln
 405 410 415
 Phe Phe Gly Val Glu
 420

<210> 659
 <211> 570
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(547)
 <223> RXA02517

<400> 659
 cgacagcaag agcatctttc tatctctata acaccttcga agaaatcgac cgcctcgcg 60
 cagcgatcga gaaggccaag caattctttg gagttgagta atg aac ctt gag cag 115
 Met Asn Leu Glu Gln
 1 5
 atg tac cag gag gtg atc ctg gac cac tac aaa aac cca cag cac aag 163
 Met Tyr Gln Glu Val Ile Leu Asp His Tyr Lys Asn Pro Gln His Lys
 10 15 20
 ggc ctt cgg gat cct ttc gat gct gag gtt cac cac gtc aac cct tct 211
 Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His His Val Asn Pro Ser
 25 30 35
 tgt ggc gac gaa ttg act ctg cgc gtg aag ctg tct gag gac ggc tcc 259
 Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu Ser Glu Asp Gly Ser
 40 45 50
 acc gtg gag gac gtc tcc tac gaa gca gtt ggt tgc tca atc agc cag 307
 Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly Cys Ser Ile Ser Gln
 55 60 65
 gcc tcc acg tcc gtt atg gcc gag gag atc gtg ggc caa ccc gtc gac 355
 Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val Gly Gln Pro Val Asp
 70 75 80 85
 aag gcg ctg gaa aag ctc aca gaa ttt gag aag atg atc gtt tcc cgc 403
 Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys Met Ile Val Ser Arg
 90 95 100
 ggt cag ttt gtt ggc gat gaa gat ctc atc gga gat ggc gtt gct ttc 451
 Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly Asp Gly Val Ala Phe
 105 110 115

tcc gga gtc gcc aag tac ccg gca cgc gtg aag tgc gcg ctg ctt ggg 499
 Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys Cys Ala Leu Leu Gly
 120 125 130

tgg aag gct ttc cag gcg gca acc gct gac gct gtt gcg cac gca cat 547
 Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala Val Ala His Ala His
 135 140 145

tagcccgctg tattaattgg agg 570

<210> 660

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

Met Asn Leu Glu Gln Met Tyr Gln Glu Val Ile Leu Asp His Tyr Lys
 1 5 10 15

Asn Pro Gln His Lys Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His
 20 25 30

His Val Asn Pro Ser Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu
 35 40 45

Ser Glu Asp Gly Ser Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly
 50 55 60

Cys Ser Ile Ser Gln Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val
 65 70 75 80

Gly Gln Pro Val Asp Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys
 85 90 95

Met Ile Val Ser Arg Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly
 100 105 110

Asp Gly Val Ala Phe Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys
 115 120 125

Cys Ala Leu Leu Gly Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala
 130 135 140

Val Ala His Ala His
 145

<210> 661

<211> 1167

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1144)

<223> RXA01747

<400> 661

cgaagtagag ccgattgcag aatcggcgga atgagacgtc gaaaagcggt taagctttcc 60

ctaaaaatat cactaactcg aaagatgtaa ggttgcat											gtg	act	atc	gca	cct	115	
											Val	Thr	Ile	Ala	Pro		
											1				5		
gaa	gga	cga	cga	ctg	cta	cgc	gtc	gaa	gct	cga	aac	tca	gaa	acc	ccg	163	
Glu	Gly	Arg	Arg	Leu	Leu	Arg	Val	Glu	Ala	Arg	Asn	Ser	Glu	Thr	Pro		
				10					15					20			
att	gag	acg	aag	cct	cga	tgg	att	aga	aac	cag	gtc	aaa	aac	gga	cct	211	
Ile	Glu	Thr	Lys	Pro	Arg	Trp	Ile	Arg	Asn	Gln	Val	Lys	Asn	Gly	Pro		
				25					30					35			
gag	tat	cag	gat	atg	aag	gaa	cgt	gtc	gct	ggc	gca	tca	cta	cac	act	259	
Glu	Tyr	Gln	Asp	Met	Lys	Glu	Arg	Val	Ala	Gly	Ala	Ser	Leu	His	Thr		
				40					45					50			
gtg	tgt	cag	gag	gct	ggc	tgt	cct	aat	atc	cat	gag	tgt	tgg	gaa	tcc	307	
Val	Cys	Gln	Glu	Ala	Gly	Cys	Pro	Asn	Ile	His	Glu	Cys	Trp	Glu	Ser		
		55			60						65						
cgt	gag	gca	acc	ttc	ctc	att	ggt	ggc	gcc	aac	tgc	tct	cgc	cgc	tgt	355	
Arg	Glu	Ala	Thr	Phe	Leu	Ile	Gly	Gly	Ala	Asn	Cys	Ser	Arg	Arg	Cys		
70						75					80					85	
gat	ttc	tgc	atg	atc	aac	tcg	gct	cgc	cct	gag	cca	ctc	gac	cgc	ggt	403	
Asp	Phe	Cys	Met	Ile	Asn	Ser	Ala	Arg	Pro	Glu	Pro	Leu	Asp	Arg	Gly		
				90					95					100			
gag	cca	ctg	cgt	gtc	gct	gag	tct	gtt	cgt	gag	atg	cag	ctg	aat	tac	451	
Glu	Pro	Leu	Arg	Val	Ala	Glu	Ser	Val	Arg	Glu	Met	Gln	Leu	Asn	Tyr		
				105					110					115			
tcc	acc	atc	acc	ggt	gtt	acc	cgt	gat	gat	ctg	gat	gat	gaa	ggc	gca	499	
Ser	Thr	Ile	Thr	Gly	Val	Thr	Arg	Asp	Asp	Leu	Asp	Asp	Glu	Gly	Ala		
				120					125					130			
tgg	ctg	tac	tca	gaa	gtg	gtt	cgt	aag	atc	cac	gag	ctg	aac	cca	cac	547	
Trp	Leu	Tyr	Ser	Glu	Val	Val	Arg	Lys	Ile	His	Glu	Leu	Asn	Pro	His		
				135					140					145			
acc	ggt	gtg	gaa	aac	ctg	gtg	cct	gat	ttc	tcc	ggc	aag	aag	gat	ctg	595	
Thr	Gly	Val	Glu	Asn	Leu	Val	Pro	Asp	Phe	Ser	Gly	Lys	Lys	Asp	Leu		
150				155						160				165			
ctg	cag	gaa	gtt	ttt	gaa	tcc	cgc	cca	gag	gtt	ttc	gct	cac	aac	gtg	643	
Leu	Gln	Glu	Val	Phe	Glu	Ser	Arg	Pro	Glu	Val	Phe	Ala	His	Asn	Val		
				170					175					180			
gaa	act	gtg	cca	cgt	att	ttc	aag	cgc	att	cgc	cca	gca	ttc	cgc	tac	691	
Glu	Thr	Val	Pro	Arg	Ile	Phe	Lys	Arg	Ile	Arg	Pro	Ala	Phe	Arg	Tyr		
				185					190					195			
gag	cgt	tca	ctt	gat	gtg	atc	cgt	cag	gct	cgc	gat	ttc	ggt	ctg	gtg	739	
Glu	Arg	Ser	Leu	Asp	Val	Ile	Arg	Gln	Ala	Arg	Asp	Phe	Gly	Leu	Val		
				200					205					210			
acc	aag	tcc	aac	ctg	att	ttg	ggc	atg	ggt	gaa	acc	aag	gaa	gaa	atc	787	
Thr	Lys	Ser	Asn	Leu	Ile	Leu	Gly	Met	Gly	Glu	Thr	Lys	Glu	Glu	Ile		
215				220						225							

acc gag gcg ctg cag gat ctg cac gac gct ggc tgt gac atc atc acc 835
 Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr
 230 235 240 245

 atc acc cag tac ctg cgt cct ggt cct ttg ttc cac ccc atc gag cgt 883
 Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe His Pro Ile Glu Arg
 250 255 260

 tgg gtg aag cct gag gag ttc ctc gag cac gct gat gct gca aag gaa 931
 Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala Asp Ala Ala Lys Glu
 265 270 275

 atg ggc ttc gct gct gtt atg tcc ggc cca ttg gtt cgt tcc tct tac 979
 Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr
 280 285 290

 cgt gca ggc cgt ctg tac gcg cag gcc atg gag ttc cgt ggc gag gaa
 1027
 Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu Phe Arg Gly Glu Glu
 295 300 305

 atc cca gca cac ctc gcg cac ctg aag gat act tcc gga gga tcc acc
 1075
 Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr
 310 315 320 325

 gcc cag gaa gca tct aca ctt ctg gag cgt tac ggt gct tcc gaa gac
 1123
 Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr Gly Ala Ser Glu Asp
 330 335 340

 acc cca gtg gtg tcc ttc aac taagcccgaa gttttttaac cgc
 1167
 Thr Pro Val Val Ser Phe Asn
 345

<210> 662

<211> 348

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 662

Val Thr Ile Ala Pro Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg
 1 5 10 15

 Asn Ser Glu Thr Pro Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln
 20 25 30

 Val Lys Asn Gly Pro Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly
 35 40 45

 Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His
 50 55 60

 Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn
 65 70 75 80

 Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu
 85 90 95

Pro Leu Asp Arg Gly Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu
 100 105 110
 Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
 115 120 125
 Asp Asp Glu Gly Ala Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His
 130 135 140
 Glu Leu Asn Pro His Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
 145 150 155 160
 Gly Lys Lys Asp Leu Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val
 165 170 175
 Phe Ala His Asn Val Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg
 180 185 190
 Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg
 195 200 205
 Asp Phe Gly Leu Val Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu
 210 215 220
 Thr Lys Glu Glu Ile Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly
 225 230 235 240
 Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe
 245 250 255
 His Pro Ile Glu Arg Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala
 260 265 270
 Asp Ala Ala Lys Glu Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu
 275 280 285
 Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu
 290 295 300
 Phe Arg Gly Glu Glu Ile Pro Ala His Leu Ala His Leu Lys Asp Thr
 305 310 315 320
 Ser Gly Gly Ser Thr Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr
 325 330 335
 Gly Ala Ser Glu Asp Thr Pro Val Val Ser Phe Asn
 340 345

<210> 663

<211> 876

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(853)

<223> RXA01746

<400> 663

aaaccgccac tcccctttca ctggggagtg gcggttttgt cgtttcatgc atgcagtgtg 60

tgacttatca accttgtag ggctaggggtg gatatctatc atg act gca cca aga	115
Met Thr Ala Pro Arg	
1 5	
gat cct ttt ttc ccc gca gat ctt tct atc cgc gcg tct gca gag ccc	163
Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg Ala Ser Ala Glu Pro	
10 15 20	
att gaa att cag cgg ttg ggt ttg atc gat tat caa gag gcc tgg gat	211
Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr Gln Glu Ala Trp Asp	
25 30 35	
tat caa gca gag ctt gct acc cgt agg gct aat gat gaa atc cct gat	259
Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn Asp Glu Ile Pro Asp	
40 45 50	
cag ctg ctt att ttg gag cac ccg tcg gtg tat acc gca ggt aag cgc	307
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg	
55 60 65	
acc cag ccg gaa gat ctt ccc acc aac gga ctg ccg gtg atc aat gct	355
Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu Pro Val Ile Asn Ala	
70 75 80 85	
gat cgt ggt ggt cgc atc acg tgg cat ggt cct ggc caa ttg gtg atc	403
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro Gly Gln Leu Val Ile	
90 95 100	
tat ccg atc atc aaa tta gcc gat ccg atc gat gtg gtt gat tac gta	451
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp Val Val Asp Tyr Val	
105 110 115	
aga cgc ctc gag gaa gcg ctc atc caa gtt gtc ggc gat atg ggt gtt	499
Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val Gly Asp Met Gly Val	
120 125 130	
gcc ggc gct ggg cgc att gat ggg cgt tcg ggt gtg tgg gtg cca gct	547
Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala	
135 140 145	
cat gat ggt tgg gtg gac agc aag gtt gcg gcc atc ggc att cga ata	595
His Asp Gly Trp Val Asp Ser Lys Val Ala Ala Ile Gly Ile Arg Ile	
150 155 160 165	
act cgt ggt gtt gca atg cac ggt gtg gcc atc aac tgc aac aac acg	643
Thr Arg Gly Val Ala Met His Gly Val Ala Ile Asn Cys Asn Asn Thr	
170 175 180	
ttg gat ttc tat gag cac atc att ccg tgt ggc att gct gat gca ggc	691
Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly Ile Ala Asp Ala Gly	
185 190 195	
ttg agc aca ctc tcg agg gaa ctg aaa agg gac gtt tca gtt gag gaa	739
Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp Val Ser Val Glu Glu	
200 205 210	
tta gtc gag cca tcg atc cgc gca ttg gat gat gct ttg gct ggt cgg	787
Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp Ala Leu Ala Gly Arg	
215 220 225	

ctg gtt gtt tct gat cat tct ttc ggc agc gcg ccc gac cca act aag 835
 Leu Val Val Ser Asp His Ser Phe Gly Ser Ala Pro Asp Pro Thr Lys
 230 235 240 245

aat ctc cct aaa cgg ggg tagtacgagg aattttgtcg gtg 876
 Asn Leu Pro Lys Arg Gly
 250

<210> 664

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 664

Met Thr Ala Pro Arg Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg
 1 5 10 15

Ala Ser Ala Glu Pro Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr
 20 25 30

Gln Glu Ala Trp Asp Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn
 35 40 45

Asp Glu Ile Pro Asp Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr
 50 55 60

Thr Ala Gly Lys Arg Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu
 65 70 75 80

Pro Val Ile Asn Ala Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro
 85 90 95

Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp
 100 105 110

Val Val Asp Tyr Val Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val
 115 120 125

Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly
 130 135 140

Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala
 145 150 155 160

Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile
 165 170 175

Asn Cys Asn Asn Thr Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly
 180 185 190

Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp
 195 200 205

Val Ser Val Glu Glu Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp
 210 215 220

Ala Leu Ala Gly Arg Leu Val Val Ser Asp His Ser Phe Gly Ser Ala
 225 230 235 240

Pro Asp Pro Thr Lys Asn Leu Pro Lys Arg Gly

245

250

```
<210> 665
<211> 1179
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1156)  
<223> RXA02106
```

<400> 665																	
ggtcgccgct tttcgacgcc cgcctgcggc gggatgactg tgatggaggg gcgcgctcgac																	60
aagcaaaaatc tcttttagcaa attcgggttac tgtgggggcgc atg aat aac cat ttt																	115
Met Asn Asn His Phe																	5
gag ctc aaa gta cct ggt gga aag ctt gtc gtc gtt gat gtg acc acc																	163
Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val Val Asp Val Thr Thr																	20
gat ctg gat tcc att gct gac gtg aag att tcc ggc gat ttc ttc ctc																	211
Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser Gly Asp Phe Phe Leu																	35
gaa ccc gat gag gca ttc ttc gcc ctt ggc cgg gcg ctg cag ggg gcg																	259
Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg Ala Leu Gln Gly Ala																	50
tcg gtg ggt gat aac act gat cgt ttg cag gca aag ttg gat gca gcg																	307
Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala Lys Leu Asp Ala Ala																	65
ttg gcg gaa tat gat gac gtt gag cta cac ggc ttt agc act gcg gat																	355
Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly Phe Ser Thr Ala Asp																	85
att gct tta gct gtg cgt cgg gca gtc acc ggc gcg caa gat ttc acc																	403
Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly Ala Gln Asp Phe Thr																	100
gat tat gaa tgg gaa atc ctg cac cca ggg gtg ctt cct acc cca ctt																	451
Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val Leu Pro Thr Pro Leu																	115
aac gtt gcg ttg gat gag ctc ctt ttg gac caa gtt gcc agt ggt cag																	499
Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln Val Ala Ser Gly Gln																	130
cgt ggc ccg acg atg cgc att tgg gat tgg gat gat cgc gcc aca gtg																	547
Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp Asp Arg Ala Thr Val																	145
atc ggt agt ttc cag tca tat gtc aat gaa atc aac caa gaa ggc gtt																	595
Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile Asn Gln Glu Gly Val																	165
aat gaa cat ggt gtg acc gtg gta cga cgc atg tct ggt ggc ggt gca																	643

Asn	Glu	His	Gly	Val	Thr	Val	Val	Arg	Arg	Met	Ser	Gly	Gly	Gly	Ala		
				170					175						180		
atg	ttt	atg	gag	ggc	ggc	aac	tgc	atc	acc	tat	tcc	ctg	tat	gca	ccg	691	
Met	Phe	Met	Glu	Gly	Gly	Asn	Cys	Ile	Thr	Tyr	Ser	Leu	Tyr	Ala	Pro		
			185				190					195					
gaa	tct	ctc	gtt	gct	ggc	ttg	agc	tat	gag	cag	tcc	tat	gaa	tat	ttg	739	
Glu	Ser	Leu	Val	Ala	Gly	Leu	Ser	Tyr	Glu	Gln	Ser	Tyr	Glu	Tyr	Leu		
		200				205					210						
gat	cgt	tgg	gtg	att	gct	gcg	ctg	aag	aca	cac	gat	gtt	gac	gct	tgg	787	
Asp	Arg	Trp	Val	Ile	Ala	Ala	Leu	Lys	Thr	His	Asp	Val	Asp	Ala	Trp		
	215				220				225								
tac	gtg	cct	atc	aat	gac	atc	acc	tcc	acc	ggc	gga	aaa	atc	ggc	ggc	835	
Tyr	Val	Pro	Ile	Asn	Asp	Ile	Thr	Ser	Thr	Gly	Gly	Lys	Ile	Gly	Gly		
230				235					240					245			
gct	gca	cag	aaa	cgt	cgc	agt	ggc	gca	gtc	ctc	cac	cac	gtg	acc	atg	883	
Ala	Ala	Gln	Lys	Arg	Arg	Ser	Gly	Ala	Val	Leu	His	His	Val	Thr	Met		
			250				255						260				
tcc	tat	gac	atc	gat	gcg	gac	atg	atg	acc	cag	gtg	ttg	cgc	att	gga	931	
Ser	Tyr	Asp	Ile	Asp	Ala	Asp	Met	Met	Thr	Gln	Val	Leu	Arg	Ile	Gly		
		265					270					275					
aag	gtg	aag	att	tcc	gac	aag	ggc	ctt	cgc	agc	gca	aag	aag	cgc	gtt	979	
Lys	Val	Lys	Ile	Ser	Asp	Lys	Gly	Leu	Arg	Ser	Ala	Lys	Lys	Arg	Val		
	280					285					290						
gat	cct	ctg	cgc	cgc	caa	aca	ggc	gca	tca	cgt	gag	caa	atc	atc	gac		
1027																	
Asp	Pro	Leu	Arg	Arg	Gln	Thr	Gly	Ala	Ser	Arg	Glu	Gln	Ile	Ile	Asp		
	295				300						305						
acc	cta	aag	tcc	aca	ttc	agt	gct	agg	tac	ggc	gcg	caa	gaa	gta	gag		
1075																	
Thr	Leu	Lys	Ser	Thr	Phe	Ser	Ala	Arg	Tyr	Gly	Ala	Gln	Glu	Val	Glu		
310				315				320					325				
ctc	agc	gat	gaa	gat	ttc	gcg	gca	ggc	cac	gac	cta	gta	aaa	acc	aaa		
1123																	
Leu	Ser	Asp	Glu	Asp	Phe	Ala	Ala	Gly	His	Asp	Leu	Val	Lys	Thr	Lys		
			330				335						340				
tac	gcc	acc	gag	gag	tgg	act	aag	cga	gtt	caa	tagttttctat	ggatctgcac					
1176																	
Tyr	Ala	Thr	Glu	Glu	Trp	Thr	Lys	Arg	Val	Gln							
		345					350										

aag
1179

<210> 666

<211> 352

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 666

Met Asn Asn His Phe Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val
 1 5 10 15
 Val Asp Val Thr Thr Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser
 20 25 30
 Gly Asp Phe Phe Leu Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg
 35 40 45
 Ala Leu Gln Gly Ala Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala
 50 55 60
 Lys Leu Asp Ala Ala Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly
 65 70 75 80
 Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly
 85 90 95
 Ala Gln Asp Phe Thr Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val
 100 105 110
 Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln
 115 120 125
 Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp
 130 135 140
 Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile
 145 150 155 160
 Asn Gln Glu Gly Val Asn Glu His Gly Val Thr Val Val Arg Arg Met
 165 170 175
 Ser Gly Gly Gly Ala Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr
 180 185 190
 Ser Leu Tyr Ala Pro Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln
 195 200 205
 Ser Tyr Glu Tyr Leu Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His
 210 215 220
 Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly
 225 230 235 240
 Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu
 245 250 255
 His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln
 260 265 270
 Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser
 275 280 285
 Ala Lys Lys Arg Val Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg
 290 295 300
 Glu Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly
 305 310 315 320
 Ala Gln Glu Val Glu Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp

325 330 335
 Leu Val Lys Thr Lys Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
 340 345 350

<210> 667
 <211> 403
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(403)
 <223> RXS01183

<400> 667
 cttgatatga cccgaacacc acacatcaca aattgaatcg gtatcctttg ggggtattagt 60
 ttccggtttta acgacacgac ttgcgaggag tcttaaaata atg gcg ttc tcc gta 115
 Met Ala Phe Ser Val
 1 5
 gag atg ccc gag ctg ggc gaa tca gta acc gaa ggc acg atc acc cag 163
 Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln
 10 15 20
 tgg ttg aag tct gtt ggt gac act gtt gag gta gat gag ccg ttg ctc 211
 Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu
 25 30 35
 gag gtc tca act gac aag gtc gac acc gag att ccc tct cct gtc gcc 259
 Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala
 40 45 50
 ggt gtc atc cta gag att aag gct gaa gag gat gac acc gtc gac gtc 307
 Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp Asp Thr Val Asp Val
 55 60 65
 ggc ggt gtc att gca ata atc ggc gat gct gat gag act cct gcc aac 355
 Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp Glu Thr Pro Ala Asn
 70 75 80 85
 gaa gct cct gcc gac gag gca cca gct cct gcc gaa gag gaa gaa cca 403
 Glu Ala Pro Ala Asp Glu Ala Pro Ala Pro Ala Glu Glu Glu Glu Pro
 90 95 100

<210> 668
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 668
 Met Ala Phe Ser Val Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu
 1 5 10 15
 Gly Thr Ile Thr Gln Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val

	20		25		30										
Asp	Glu	Pro	Leu	Leu	Glu	Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile
	35						40					45			
Pro	Ser	Pro	Val	Ala	Gly	Val	Ile	Leu	Glu	Ile	Lys	Ala	Glu	Glu	Asp
	50					55					60				
Asp	Thr	Val	Asp	Val	Gly	Gly	Val	Ile	Ala	Ile	Ile	Gly	Asp	Ala	Asp
65					70					75					80
Glu	Thr	Pro	Ala	Asn	Glu	Ala	Pro	Ala	Asp	Glu	Ala	Pro	Ala	Pro	Ala
				85					90						95
Glu	Glu	Glu	Glu	Pro											
				100											

<210> 669

<211> 1305

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1282)

<223> RXS01260

<400> 669

ctaaacgtgg gctgcattcc ttccaaagtc tctgatcaaaa aacgctgaag ttgcccatatc 60

ctttacccat	gagaagaaga	ccttcggcat	caatggcgaa	gtg	acc	ttc	aac	tat	115
				Val	Thr	Phe	Asn	Tyr	
				1				5	

gag	gat	gct	cac	aag	cgt	tcc	cgt	ggc	gtt	tcc	gac	aag	atc	gtt	gga	163
Glu	Asp	Ala	His	Lys	Arg	Ser	Arg	Gly	Val	Ser	Asp	Lys	Ile	Val	Gly	
				10					15					20		

ggc	gtt	cat	tac	ttg	atg	aag	aag	aac	aag	atc	atc	gaa	att	cat	ggc	211
Gly	Val	His	Tyr	Leu	Met	Lys	Lys	Asn	Lys	Ile	Ile	Glu	Ile	His	Gly	
			25					30					35			

ctt	gga	aac	ttc	aag	gat	gct	aag	act	ctt	gag	gtc	acc	gac	ggc	aag	259
Leu	Gly	Asn	Phe	Lys	Asp	Ala	Lys	Thr	Leu	Glu	Val	Thr	Asp	Gly	Lys	
		40					45					50				

gat	gct	ggc	aag	acc	atc	acc	ttt	gat	gac	tgc	atc	atc	gca	acc	ggc	307
Asp	Ala	Gly	Lys	Thr	Ile	Thr	Phe	Asp	Asp	Cys	Ile	Ile	Ala	Thr	Gly	
	55					60					65					

tcg	gta	gtc	aac	acc	ctc	cgt	ggc	gtt	gac	ttc	tca	gag	aac	gtt	gtg	355
Ser	Val	Val	Asn	Thr	Leu	Arg	Gly	Val	Asp	Phe	Ser	Glu	Asn	Val	Val	
	70				75					80				85		

tct	ttt	gaa	gag	cag	att	ctt	aac	cct	gtt	gcg	cca	aag	aag	atg	gtc	403
Ser	Phe	Glu	Glu	Gln	Ile	Leu	Asn	Pro	Val	Ala	Pro	Lys	Lys	Met	Val	
				90				95						100		

att	gtt	ggc	gca	ggc	gca	att	gga	atg	gaa	ttc	gcc	tac	gtt	ctt	ggc	451
Ile	Val	Gly	Ala	Gly	Ala	Ile	Gly	Met	Glu	Phe	Ala	Tyr	Val	Leu	Gly	

	105	110	115	
aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt				499
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu				
	120	125	130	
cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag				547
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys				
	135	140	145	
aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg				595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg				
	150	155	160	165
gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac				643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp				
	170	175		180
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc				691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe				
	185	190		195
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc				739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu				
	200	205	210	
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc				787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val				
	215	220	225	
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct				835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala				
	230	235	240	245
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt				883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly				
	250	255		260
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc				931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr				
	265	270	275	
ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc				979
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala				
	280	285	290	
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc				
1027				
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe				
	295	300	305	
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca				
1075				
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala				
	310	315	320	325
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg				
1123				
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu				
	330	335		340

gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag
1171

Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln
345 350 355

aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac
1219

Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
360 365 370

cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga
1267

Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly
375 380 385

cac atg atc aac ttc tagaatccac ctcgttgcc ctg
1305

His Met Ile Asn Phe
390

<210> 670

<211> 394

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 670

Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser
1 5 10 15

Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile
20 25 30

Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu
35 40 45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys
50 55 60

Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe
65 70 75 80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala
85 90 95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
100 105 110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe
115 120 125

Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile
130 135 140

Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala
145 150 155 160

Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln
165 170 175

Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met

180					185					190					
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn
		195					200					205			
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr
	210					215					220				
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala
225					230					235					240
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala
				245					250					255	
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met
			260					265					270		
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr
		275					280					285			
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val
	290					295					300				
Ala	Ser	Phe	Pro	Phe	Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu
305					310					315					320
Thr	Asp	Gly	Phe	Ala	Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu
				325					330					335	
Leu	Gly	Ala	His	Leu	Val	Gly	Ala	Asn	Ala	Ser	Glu	Leu	Ile	Asn	Glu
			340					345					350		
Leu	Val	Leu	Ala	Gln	Asn	Trp	Asp	Leu	Thr	Thr	Glu	Glu	Ile	Ser	Arg
	355						360					365			
Ser	Val	His	Ile	His	Pro	Thr	Leu	Ser	Glu	Ala	Val	Lys	Glu	Ala	Ala
	370					375					380				
His	Gly	Ile	Ser	Gly	His	Met	Ile	Asn	Phe						
385					390										

<210> 671

<211> 294

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(271)

<223> RXS01261

<400> 671

gtgggtgttt ttcattttct tccactctaa aattaagtat ggaaaaccaa ccgcacccgg 60

atgcacgaca	atgacccact	aaacacgtat	ccttgaatgc	gtg	act	gaa	cat	tat	115
				Val	Thr	Glu	His	Tyr	
				1				5	

gac	gta	gta	gta	ctc	gga	gcc	ggc	ccc	ggg	ggc	tat	gtc	tcc	gcc	atc	163
Asp	Val	Val	Val	Leu	Gly	Ala	Gly	Pro	Gly	Gly	Tyr	Val	Ser	Ala	Ile	

	10	15	20	
cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac				211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr				
	25	30	35	
tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct				259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser				
	40	45	50	
gat caa aaa cgc tgaagttgcc cataccttta ccc				294
Asp Gln Lys Arg				
	55			

<210> 672

<211> 57

<212> PRT

<213> Corynebacterium glutamicum

<400> 672

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly				
1	5	10	15	
Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val				
	20	25	30	
Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile				
	35	40	45	
Pro Ser Lys Val Ser Asp Gln Lys Arg				
	50	55		

<210> 673

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> RXA02717

<400> 673

aggcatgtcc ctaacgaaca tcccagcctc atctcaatgg gcaattagcg acgttttgaa	60
gcgtccttca cccggccgag taccttttttc tgctcgagttt atg cca ccc cgc gac	115
	Met Pro Pro Arg Asp
	1 5
gat gca gct gaa gag cgt ctt tac cgc gca gca gag gtc ttc cat gac	163
Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp	
	10 15 20
ctc ggt gca tcg ttt gtc tcc gtg act tat ggt gct ggc gga tca acc	211
Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr	
	25 30 35
cgt gag aga acc tca cgt att gct cga cga tta gcg aaa caa ccg ttg	259
Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu	

40	45	50	
acc act ctg gtg cac ctg acc ctg gtt aac cac act cgc gaa gag atg Thr Thr Leu Val His Leu Thr Leu Val Asn His Thr Arg Glu Glu Met 55 60 65			307
aag gca att ctt cgg gaa tac cta gag ctg gga tta aca aac ctg ttg Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly Leu Thr Asn Leu Leu 70 75 80 85			355
gcg ctt cga gga gat ccg cct gga gac cca tta ggc gat tgg gtg agc Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu Gly Asp Trp Val Ser 90 95 100			403
acc gat gga gga ctg aac tat gcc tct gag ctc atc gat ctt att aag Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu Ile Asp Leu Ile Lys 105 110 115			451
tcc act cct gag ttc cgg gaa ttc gac ctc ggt atc gcc tcc ttc ccc Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly Ile Ala Ser Phe Pro 120 125 130			499
gaa ggg cat ttc cgg gcg aaa act cta gaa gaa gac acc aaa tac act Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu Asp Thr Lys Tyr Thr 135 140 145			547
ctg gcg aag ctg cgt gga ggg gca gag tac tcc atc acg cag atg ttc Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser Ile Thr Gln Met Phe 150 155 160 165			595
ttt gat gtg gaa gac tac ctg cga ctt cgt gat cgc ctt gtc gct gca Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp Arg Leu Val Ala Ala 170 175 180			643
gac ccc att cat ggt gcg aag cca atc att cct ggc atc atg ccc att Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro Gly Ile Met Pro Ile 185 190 195			691
acg agc ctg cgg tct gtg cgt cga cag gtc gaa ctc tct ggt gct caa Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu Leu Ser Gly Ala Gln 200 205 210			739
ttg ccg agc caa cta gaa gaa tca ctt gtt cga gct gca aac ggc aat Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg Ala Ala Asn Gly Asn 215 220 225			787
gaa gaa gcg aac aaa gac gag atc cgc aag gtg ggc att gaa tat tcc Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val Gly Ile Glu Tyr Ser 230 235 240 245			835
acc aat atg gca gag cga ctc att gcc gaa ggt gcg gaa gat ctg cac Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly Ala Glu Asp Leu His 250 255 260			883
ttc atg acg ctt aac ttc acc cgt gca acc caa gaa gtg ttg tac aac Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln Glu Val Leu Tyr Asn 265 270 275			931
ctt ggc atg gcg cct gct tgg gga gca gag cac ggc caa gac gcg gtg Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His Gly Gln Asp Ala Val 280 285 290			979

cgt taagccctct taggaatcat gaa
1005
Arg

<210> 674
<211> 294
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 674
Met Pro Pro Arg Asp Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala
1 5 10 15
Glu Val Phe His Asp Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly
20 25 30
Ala Gly Gly Ser Thr Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu
35 40 45
Ala Lys Gln Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Asn His
50 55 60
Thr Arg Glu Glu Met Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly
65 70 75 80
Leu Thr Asn Leu Leu Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu
85 90 95
Gly Asp Trp Val Ser Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu
100 105 110
Ile Asp Leu Ile Lys Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly
115 120 125
Ile Ala Ser Phe Pro Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu
130 135 140
Asp Thr Lys Tyr Thr Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser
145 150 155 160
Ile Thr Gln Met Phe Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp
165 170 175
Arg Leu Val Ala Ala Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro
180 185 190
Gly Ile Met Pro Ile Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu
195 200 205
Leu Ser Gly Ala Gln Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg
210 215 220
Ala Ala Asn Gly Asn Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val
225 230 235 240
Gly Ile Glu Tyr Ser Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly
245 250 255

Ala Glu Asp Leu His Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln
260 265 270

Glu Val Leu Tyr Asn Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His
275 280 285

Gly Gln Asp Ala Val Arg
290

<210> 675

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> RXN02027

<400> 675

```

tcacgtgctc atcgataggc aaactcatgg aaccaagagt acctgcccc gcaaccccaa 60
tcgtcgtagc cctccgaaaa taacggttat ccttagattt atg agc caa act aag 115
                                     Met Ser Gln Thr Lys
                                     1 5
cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
                                     10 15 20
gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
                                     25 30 35
tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
                                     40 45 50
cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
                                     55 60 65
act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
                                     70 75 80 85
tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
                                     90 95 100
atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
                                     105 110 115
tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
                                     120 125 130
agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly

```


135 140 145

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
 150 155 160 165

gat atc 601
 Asp Ile

<210> 676
 <211> 167
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 676
 Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
 1 5 10 15

Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
 20 25 30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala
 35 40 45

Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp
 50 55 60

Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu
 65 70 75 80

Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val
 85 90 95

Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro
 100 105 110

Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys
 115 120 125

Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg
 130 135 140

Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn
 145 150 155 160

Gly Glu Ile Arg Asp Asp Ile
 165

<210> 677
 <211> 595
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(595)
 <223> FRXA02027

<400> 677

tcacgtgctc atcgataggg aaactcatgg aaccaagagt acctgcccc gcaaccccaa 60

tcgtcgtacc cctccgaaaa taacggttat ccttagattt atg agc caa act aag 115
 Met Ser Gln Thr Lys
 1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
 Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
 10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
 Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
 25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
 Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
 55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
 70 75 80 85

tggt gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
 Arg Leu Gly Lys Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly
 135 140 145

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
 150 155 160 165

<210> 678

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 678

Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
 1 5 10 15

Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
 20 25 30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala

35	40	45
Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp		
50	55	60
Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu		
65	70	75
Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val		
85	90	95
Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro		
100	105	110
Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys		
115	120	125
Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg		
130	135	140
Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn		
145	150	155
Gly Glu Ile Arg Asp		
165		

<210> 679

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 679

tggagctcaa caaggcagcg tacatgtttg agtacagctt cgatgacatc accgtgtccg 60

gctacgatcc acacccattg atccgcggca aggtcgccgt	atg atc ggt gcg att	115
	Met Ile Gly Ala Ile	
	1 5	

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc	163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro	
10 15 20	

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc	211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly	
25 30 35	

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag	259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys	
40 45 50	

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc	307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly	
55 60 65	

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc	355
---	-----

Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
 70 75 80 85
 tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
 Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
 90 95 100
 gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
 105 110 115
 ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
 120 125 130
 tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
 135 140 145
 atc aag gtt taaggagcaa acaacatgag caa 579
 Ile Lys Val
 150

<210> 680

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 680

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
 1 5 10 15
 Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
 20 25 30
 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
 130 135 140
 Lys Phe Gln Arg Tyr Ile Lys Val
 145 150

```
<210> 681
<211> 1044
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1021)
<223> RXN01321
```

<400> 681																
ggaggggtgta gtcaaggatt tggggccatgg tggagcggga aatcgtcata tccataaccct																60
acttagacct gacttagtgt gggaaaatTTT ccagggtaga atg caa cga atg acc																115
Met Gln Arg Met Thr																5
1																
ccg agt tct cct gaa gtt cgt aat cgt ccg agc gct gcg cct gaa gag																163
Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser Ala Ala Pro Glu Glu																20
10 15																
cgt cag ttt gtg ctc act ttt ggc tgc cct gac tcc act gga att gtg																211
Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp Ser Thr Gly Ile Val																35
25 30																
gcg aag ttg tcg tcg ttc cta gct gag cgt ggg ggt tgg att act gag																259
Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly Gly Trp Ile Thr Glu																50
40 45																
gct gga tat ttc acg gat cct gat tcg aat tgg ttc ttt act cgt cag																307
Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp Phe Phe Thr Arg Gln																65
55 60																
gcg att cgc gct gag tcg att gat acc acg att gag cag ttg cgg gag																355
Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile Glu Gln Leu Arg Glu																85
70 75 80																
gag ttc gct ccg ctt gcg gag gag ttc ggc ccg agg gct aag tgg agt																403
Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro Arg Ala Lys Trp Ser																100
90 95																
ttc act gac act gcg cag gtg aag aag gct gtg ttg ttg gtg tct aag																451
Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val Leu Leu Val Ser Lys																115
105 110																
gag ggc cac tgc ttg cac gat ttg tta ggt cgt gtg gct gag aat gat																499
Glu Gly His Cys Leu His Asp Leu Leu Gly Arg Val Ala Glu Asn Asp																130
120 125 130																
tat ccg atg gaa gtt gtt gcg gtt gtg ggt aac cat gag aac ttg cgt																547
Tyr Pro Met Glu Val Val Ala Val Val Gly Asn His Glu Asn Leu Arg																145
135 140 145																
tat att gcg gag aac cat aat gtt ccg ttt ttc cat gtg ccg ttt cct																595
Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe His Val Pro Phe Pro																165
150 155 160																
aag gat gcg gtt ggt aag cgg aag gcg ttt gac cag gtc gct gag att																643
Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile																180
170 175 180																

gtg aat ggt tat gat ccg gat gcg att gtt ttg gct cgt ttt atg cag 691
 Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln
 185 190 195
 att ttg ccg ccg gat ttg tgt gag atg tgg gct ggt cgt gtg ttg aat 739
 Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn
 200 205 210
 att cat cac agt ttc ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat 787
 Ile His His Ser Phe Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His
 215 220 225
 cag gcg tat agc cgt ggt gtg aag ttg att ggt gcg acc tgc cat tat 835
 Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr
 230 235 240 245
 gcg act ggg gat ctg gat gat ggt ccg atc att gag cag gat gtt att 883
 Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile
 250 255 260
 cgt gtg acg cat aag gat acg ccg act gag atg cag cgt ttg ggc cgc 931
 Arg Val Thr His Lys Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg
 265 270 275
 gat gcg gag aag cag gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag 979
 Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu
 280 285 290
 gac cgg gtg ctg gtt tac ggt aac cgc acg gtt gtc ttt gat
 1021
 Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val Val Phe Asp
 295 300 305
 taaggctttt tgcttttcga cgc
 1044

<210> 682

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 682

Met Gln Arg Met Thr Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser
 1 5 10 15
 Ala Ala Pro Glu Glu Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp
 20 25 30
 Ser Thr Gly Ile Val Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly
 35 40 45
 Gly Trp Ile Thr Glu Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp
 50 55 60
 Phe Phe Thr Arg Gln Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile
 65 70 75 80
 Glu Gln Leu Arg Glu Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro
 85 90 95

Arg Ala Lys Trp Ser Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val
 100 105 110
 Leu Leu Val Ser Lys Glu Gly His Cys Leu His Asp Leu Leu Gly Arg
 115 120 125
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
 130 135 140
 His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 145 150 155 160
 His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 165 170 175
 Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 180 185 190
 Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
 195 200 205
 Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
 210 215 220
 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
 225 230 235 240
 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
 245 250 255
 Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
 260 265 270
 Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
 275 280 285
 Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
 290 295 300
 Val Phe Asp
 305

<210> 683
 <211> 582
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (23) .. (559)
 <223> FRXA01321

<400> 683
 cttgcacgat ttgttaggtc gtgtg gct gag aat gat tat ccg atg gaa gtt 52
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val
 1 5 10

gtt gcg gtt gtg ggt aac cat gag aac ttg cgt tat att gcg gag aac 100
 Val Ala Val Val Gly Asn His Glu Asn Leu Arg Tyr Ile Ala Glu Asn
 15 20 25

cat aat gtt ccg ttt ttc cat gtg ccg ttt cct aag gat gcg gtt ggt 148
 His Asn Val Pro Phe Phe His Val Pro Phe Pro Lys Asp Ala Val Gly
 30 35 40

aag cgg aag gcg ttt gac cag gtc gct gag att gtg aat ggt tat gat 196
 Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile Val Asn Gly Tyr Asp
 45 50 55

ccg gat gcg att gtt ttg gct cgt ttt atg cag att ttg ccg ccg gat 244
 Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln Ile Leu Pro Pro Asp
 60 65 70

ttg tgt gag atg tgg gct ggt cgt gtg ttg aat att cat cac agt ttc 292
 Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn Ile His His Ser Phe
 75 80 85 90

ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat cag gcg tat agc cgt 340
 Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg
 95 100 105

ggt gtg aag ttg att ggt gcg acc tgc cat tat gcg act ggg gat ctg 388
 Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr Ala Thr Gly Asp Leu
 110 115 120

gat gat ggt ccg atc att gag cag gat gtt att cgt gtg acg cat aag 436
 Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile Arg Val Thr His Lys
 125 130 135

gat acg ccg act gag atg cag cgt ttg ggc cgc gat gcg gag aag cag 484
 Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln
 140 145 150

gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag gac cgg gtg ctg gtt 532
 Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu Asp Arg Val Leu Val
 155 160 165 170

tac ggt aac cgc acg gtt gtc ttt gat taaggctttt tgcttttcga 579
 Tyr Gly Asn Arg Thr Val Val Phe Asp
 175

cgc 582

<210> 684

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 684

Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
 1 5 10 15

His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 20 25 30

His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 35 40 45

Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 50 55 60

Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
65 70 75 80

Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
85 90 95

Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
100 105 110

Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
115 120 125

Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
130 135 140

Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
145 150 155 160

Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
165 170 175

Val Phe Asp

<210> 685
<211> 975
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(952)
<223> RXA00461

<400> 685
tggtgggagg gatgacagga ttgtcgaaga taacgtgaag tgggtgttcc ggcattgtgtt 60

tgattgtaag gccttggaag aggggtggaat aatagcgggc gtg act gca atc aaa 115
Val Thr Ala Ile Lys
1 5

ctt gat gga aac tta tac cgc ggg gaa att ttc gcc gac ttg gaa cag 163
Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe Ala Asp Leu Glu Gln
10 15 20

cgc gtt gct gcg ttg aag gag aaa ggg att gtg ccg ggg ctt gcc acc 211
Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val Pro Gly Leu Ala Thr
25 30 35

gtg ctg gtg ggt gat gac cca gcg agc cac tct tac gtg aag atg aag 259
Val Leu Val Gly Asp Asp Pro Ala Ser His Ser Tyr Val Lys Met Lys
40 45 50

cat cgt gac tgt gag cag att ggt gtg aac tcg atc cgt aag gat ctg 307
His Arg Asp Cys Glu Gln Il Gly Val Asn Ser Ile Arg Lys Asp Leu
55 60 65

cct gct gat gtc acg cag gaa gag ctt ttc gct gtc atc gat gaa ctg 355
Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala Val Ile Asp Glu Leu

70	75	80	85	
aac aac gat gat tct tgc act ggt tac att gtg cag ctt cct ttg cct				403
Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val Gln Leu Pro Leu Pro	90	95	100	
aag cac ttg gac gaa aac gct gtg ctg gag cgc att gat cca gct aag				451
Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg Ile Asp Pro Ala Lys	105	110	115	
gat gct gat ggc ctg cac cct gta aac ctg ggc aag ctt gtg ctc aac				499
Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly Lys Leu Val Leu Asn	120	125	130	
gag cca gct cca ctg cca tgc acc ccg aat ggt tcc atc agc ttg ttg				547
Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly Ser Ile Ser Leu Leu	135	140	145	
cgt cgt ttc ggc gtt gag ctt gat ggc gcg aag gtt gtt gtc att ggc				595
Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys Val Val Val Ile Gly	150	155	160	165
cgt ggc gtc acc gtt ggt cgc cca att ggc ctg atg ctg acc cgc cgt				643
Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu Met Leu Thr Arg Arg	170	175	180	
tcc gag aac tcc acg gtt act ttg tgc cac act ggc acg aag gat ctg				691
Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr Gly Thr Lys Asp Leu	185	190	195	
gct gcg gag acc cgt gcg gct gac gtc atc att gct gca gct ggt cag				739
Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile Ala Ala Ala Gly Gln	200	205	210	
ccg cac atg ctg acc gca gac atg gtc aag cca ggc gca gcg gtg ctc				787
Pro His Met Leu Thr Ala Asp Met Val Lys Pro Gly Ala Ala Val Leu	215	220	225	
gat gtc ggc gtc tcc cgc aag gac ggc aag ttg ctt ggc gac gtc cac				835
Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu Leu Gly Asp Val His	230	235	240	245
ccc gac gtg tgg gaa gtc gcc ggc gcg gtc tca cca aac cca ggc ggc				883
Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser Pro Asn Pro Gly Gly	250	255	260	
gtt ggc cct ctg acc cgt gca ttc ttg gtg cac aat gtt gtc gag cgc				931
Val Gly Pro Leu Thr Arg Ala Phe Leu Val His Asn Val Val Glu Arg	265	270	275	
gct gaa aag ctg gct gga ctc taaaaacaca tgactaatcc cgg				975
Ala Glu Lys Leu Ala Gly Leu	280			

<210> 686

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 686

Val Thr Ala Ile Lys Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe
 1 5 10 15
 Ala Asp Leu Glu Gln Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val
 20 25 30
 Pro Gly Leu Ala Thr Val Leu Val Gly Asp Asp Pro Ala Ser His Ser
 35 40 45
 Tyr Val Lys Met Lys His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser
 50 55 60
 Ile Arg Lys Asp Leu Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala
 65 70 75 80
 Val Ile Asp Glu Leu Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val
 85 90 95
 Gln Leu Pro Leu Pro Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg
 100 105 110
 Ile Asp Pro Ala Lys Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly
 115 120 125
 Lys Leu Val Leu Asn Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly
 130 135 140
 Ser Ile Ser Leu Leu Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys
 145 150 155 160
 Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu
 165 170 175
 Met Leu Thr Arg Arg Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr
 180 185 190
 Gly Thr Lys Asp Leu Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile
 195 200 205
 Ala Ala Ala Gly Gln Pro His Met Leu Thr Ala Asp Met Val Lys Pro
 210 215 220
 Gly Ala Ala Val Leu Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu
 225 230 235 240
 Leu Gly Asp Val His Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser
 245 250 255
 Pro Asn Pro Gly Gly Val Gly Pro Leu Thr Arg Ala Phe Leu Val His
 260 265 270
 Asn Val Val Glu Arg Ala Glu Lys Leu Ala Gly Leu
 275 280

<210> 687

<211> 711

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(688)

<223> RXA01514

<400> 687

```

accacagaaa tgcctgtcgt tccagatcag cccatcgatg gtgattccgg gaagtcgct 60
gagggcacac aggagaatcc ggaaaatgaa ggagacaacc gtg gat aac cac gct 115
Val Asp Asn His Ala
1 5
gca gtt cgc gag ttc gat gag gag cgc gca aca gct gcg att cgt gag 163
Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr Ala 1 Ala Ile Arg Glu
10 15 20
ttg ctc atc gct gtg ggt gag gat cca gat cgc gaa ggc ctg ttg gaa 211
Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg Glu Gly Leu Leu Glu
25 30 35
acc cca gct cga gtg gct agg gcg tac aag gaa act ttc gcg ggt ctg 259
Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu Thr Phe Ala Gly Leu
40 45 50
cat gag gat ccc acc act gtg ctg gag aag acg ttc tct gag ggc cat 307
His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr Phe Ser Glu Gly His
55 60 65
gaa gag ttg gtt ctg gtt cgt gag atc ccg att tac tcc atg tgt gag 355
Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile Tyr Ser Met Cys Glu
70 75 80 85
cac cac ttg gtg ccg ttc ttt ggc gtg gcg cac att ggt tac att ccg 403
His His Leu Val Pro Phe Phe Gly Val Ala His Ile Gly Tyr Ile Pro
90 95 100
ggt aag tcc ggc aag gtg act ggc ctg tcc aag ctg gcg cgt tta gcg 451
Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys Leu Ala Arg Leu Ala
105 110 115
gat atg ttt gct aag cga cct cag gtt cag gag cgc ttg acc tcc caa 499
Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu Arg Leu Thr Ser Gln
120 125 130
att gcg gat gct ctc gtc gaa aag ctt gat gcc cag gcc gtg gcc gtg 547
Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala Gln Ala Val Ala Val
135 140 145
gtg att gaa gct gag cac ctg tgc atg gcc atg cgc gga atc cgt aag 595
Val Ile Glu Ala Glu His Leu Cys Met Ala Met Arg Gly Ile Arg Lys
150 155 160 165
cct ggt gct gtg acc acg acg tct gcg gtg cgc ggc ggt ttt aag aac 643
Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg Gly Gly Phe Lys Asn
170 175 180
aac gct gcc tcc cgc gct gag gtg ttc tcc ctg att cgg ggg cac 688
Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu Ile Arg Gly His
185 190 195
taa atgaacg tatcctcttt gac 711

```

<210> 688
 <211> 196
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 688

```

Val Asp Asn His Ala Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr
  1          5          10          15

Ala Ala Ile Arg Glu Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg
          20          25          30

Glu Gly Leu Leu Glu Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu
          35          40          45

Thr Phe Ala Gly Leu His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr
  50          55          60

Phe Ser Glu Gly His Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile
  65          70          75          80

Tyr Ser Met Cys Glu His His Leu Val Pro Phe Phe Gly Val Ala His
          85          90          95

Ile Gly Tyr Ile Pro Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys
          100          105          110

Leu Ala Arg Leu Ala Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu
          115          120          125

Arg Leu Thr Ser Gln Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala
          130          135          140

Gln Ala Val Ala Val Val Ile Glu Ala Glu His Leu Cys Met Ala Met
          145          150          155          160

Arg Gly Ile Arg Lys Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg
          165          170          175

Gly Gly Phe Lys Asn Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu
          180          185          190

Ile Arg Gly His
          195
  
```

<210> 689
 <211> 513
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(490)
 <223> RXA01516

<400> 689

```

tctgcacata tgggagcatg ggggtgtgctg gtgcacgatg tcccagtatc aagggacgct 60

gttgatgttg ccgcattgtg gcgaagtggg ggaactcacc atg gct gat cgt att 115
  
```

	Met	Ala	Asp	Arg	Ile	
	1				5	
gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt						163
Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe						
	10			15	20	
gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg						211
Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met						
	25			30	35	
gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat						259
Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp						
	40			45	50	
tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc						307
Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser						
	55			60	65	
agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg						355
Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met						
	70			75	80	85
gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc						403
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro						
	90			95	100	
aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga						451
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg						
	105			110	115	
cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc						500
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala						
	120			125	130	
agttttgtcc atc						513

<210> 690

<211> 130

<212> PRT

<213> Corynebacterium glutamicum

<400> 690

Met	Ala	Asp	Arg	Ile	Glu	Leu	Lys	Gly	Leu	Glu	Cys	Phe	Gly	His	His
1				5					10					15	
Gly	Val	Phe	Asp	Phe	Glu	Lys	Glu	Gln	Gly	Gln	Pro	Phe	Ile	Val	Asp
			20					25					30		
Val	Thr	Cys	Trp	Met	Asp	Phe	Asp	Ala	Ala	Gly	Ala	Ser	Asp	Asp	Leu
		35					40					45			
Ser	Asp	Thr	Val	Asp	Tyr	Gly	Ala	Leu	Ala	Leu	Leu	Val	Ala	Glu	Ile
	50					55					60				
Val	Glu	Gly	Pro	Ser	Arg	Asp	Leu	Ile	Glu	Thr	Val	Ala	Thr	Glu	Ser
	65				70					75					80
Ala	Asp	Ala	Val	Met	Ala	Lys	Phe	Asp	Ala	Leu	His	Ala	Val	Glu	Val
				85					90					95	

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser
 115 120 125

Asn Ala
 130

<210> 691

<211> 975

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(952)

<223> RXA01515

<400> 691

taagcctggg gctgtgacca cgacgtctgc ggtgcgcggc gggtttaaga acaacgctgc 60

ctcccgcgct gaggtgttct ccctgattcg ggggcactaa atg aac gta tcc tct 115
 Met Asn Val Ser Ser
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr
 10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu
 105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
 120 125 130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547

Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
 135 140 145
 gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
 150 155 160 165
 gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
 170 175 180
 gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
 185 190 195
 cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
 200 205 210
 ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
 215 220 225
 cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
 230 235 240 245
 gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
 250 255 260
 gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
 265 270 275
 agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975
 Ser Gly Gly Thr His His Gly
 280
 <210> 692
 <211> 284
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 692
 Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly
 1 5 10 15
 Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile
 20 25 30
 Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80

Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala
85 90 95

Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp
100 105 110

Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu
115 120 125

Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly
130 135 140

Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val
145 150 155 160

His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val
165 170 175

Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser
180 185 190

Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser
195 200 205

Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala
210 215 220

Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp
225 230 235 240

Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp
245 250 255

Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val
260 265 270

Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly
275 280

<210> 693

<211> 859

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA02024

<400> 693

cactgatgac ctggatcagg ccgtcaaatt catcgtcgat gcacacgctg gattggacgt 60

agcgcgtctc cacaattaag cagtggctac attaggtggt atg agt tct ttg ccg 115
Met Ser Ser Leu Pro
1 5

gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag 163
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys
10 15 20

ggt gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val	
25 30 35	
att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly	
40 45 50	
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro	
55 60 65	
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val	
70 75 80 85	
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala	
90 95 100	
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln	
105 110 115	
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg	499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly	
120 125 130	
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val	
135 140 145	
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg	
150 155 160 165	
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe	
170 175 180	
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu	
185 190 195	
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat	739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp	
200 205 210	
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc	787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly	
215 220 225	
acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt	835
Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe	
230 235 240 245	
cgc gtg cat gaa gtt gcg gaa acc	859
Arg Val His Glu Val Ala Glu Thr	
250	

<210> 694
 <211> 253
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 694
 Met Ser Ser Leu Pro Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp
 1 5 10 15
 Ser Phe Tyr Asp Lys Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn
 20 25 30
 Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly
 35 40 45
 Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile
 50 55 60
 Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp
 65 70 75 80
 Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala
 85 90 95
 Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp
 100 105 110
 His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys
 115 120 125
 Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His
 130 135 140
 Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala
 145 150 155 160
 Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp
 165 170 175
 Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu
 180 185 190
 Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala
 195 200 205
 Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp
 210 215 220
 Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg
 225 230 235 240
 Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr
 245 250

<210> 695
 <211> 579
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 695

```

tggagctcaa caaggcagcg tacatgtttg agtacagctt cgatgacatc accgtgtccg 60
gctacgatcc acacccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115
                                         Met Ile Gly Ala Ile
                                         1 5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
                        10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
                        25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
                        40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
                        55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
                        70 75 80 85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
                        90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
                        105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
                        120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
                        135 140 145

atc aag gtt taaggagcaa acaacatgag caa 579
Ile Lys Val
150

```

<210> 696

<211> 152

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 696

```

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
  1 5 10 15

```

Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
 20 25 30
 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
 130 135 140
 Lys Phe Gln Arg Tyr Ile Lys Val
 145 150

<210> 697

<211> 1556

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1533)

<223> RXA00989

<400> 697

gga att ggc cta gtg gct aac aac gac gga atc ttt gat tcc gaa aat 48
 Gly Ile Gly Leu Val Ala Asn Asn Asp Gly Ile Phe Asp Ser Glu Asn
 1 5 10 15
 gat gac atc acc gta ggc gat gtc acg ttg ggc gag act gga ctg tct 96
 Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser
 20 25 30
 ttg ccc atc gat ctc gcc ggt gag gta gaa gca cct gcc tcc gag gag 144
 Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu
 35 40 45
 atc acc caa gaa gat ttg ctg cgc ctt gcc cag gtg gaa gca gag ttg 192
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu
 50 55 60
 gat caa cgt tgg ttg gaa acc aaa att gat ccc act ttc cga cgc atg 240
 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met
 65 70 75 80
 agc tac atg atg gat ctc atg ggc caa cca cag aat tcc ttc cca gca 288
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala

85										90					95					
att	cac	gtg	gct	ggc	acc	aac	ggt	aag	acc	tcc	acc	acc	cgc	atg	atc	336				
Ile	His	Val	Ala	Gly	Thr	Asn	Gly	Lys	Thr	Ser	Thr	Thr	Arg	Met	Ile					
		100						105					110							
gag	tcg	ttg	ctg	cgc	gca	ttc	cac	cgc	cgc	acc	ggc	cgg	acc	acc	agc	384				
Glu	Ser	Leu	Leu	Arg	Ala	Phe	His	Arg	Arg	Thr	Gly	Arg	Thr	Thr	Ser					
		115					120					125								
ccg	cac	ctg	cag	ctg	gta	acc	gaa	cgc	atc	gcg	att	gat	ggc	aag	ccc	432				
Pro	His	Leu	Gln	Leu	Val	Thr	Glu	Arg	Ile	Ala	Ile	Asp	Gly	Lys	Pro					
		130				135					140									
atc	cac	ccg	cgt	gat	ttc	gtg	cgg	atc	tac	gaa	gag	att	aag	ccc	tac	480				
Ile	His	Pro	Arg	Asp	Phe	Val	Arg	Ile	Tyr	Glu	Glu	Ile	Lys	Pro	Tyr					
145					150					155					160					
atg	gag	atg	acc	gac	gcc	tgg	tca	gag	gcc	gag	ggc	gga	ccg	aag	atg	528				
Met	Glu	Met	Thr	Asp	Ala	Trp	Ser	Glu	Ala	Glu	Gly	Gly	Pro	Lys	Met					
				165				170						175						
agc	aag	ttt	gag	gca	ctc	gtg	gcc	ctc	gct	tac	gca	ggt	ttt	gcc	gac	576				
Ser	Lys	Phe	Glu	Ala	Leu	Val	Ala	Leu	Ala	Tyr	Ala	Gly	Phe	Ala	Asp					
			180					185					190							
gct	cct	gtt	gac	gtc	gcc	gtc	gtt	gag	gtt	ggt	ctt	ggc	gga	cgc	tgg	624				
Ala	Pro	Val	Asp	Val	Ala	Val	Val	Glu	Val	Gly	Leu	Gly	Gly	Arg	Trp					
		195					200					205								
gat	gcc	act	aac	gtg	atc	aac	gca	gct	gtt	tcc	gtg	atc	acc	ccg	gtg	672				
Asp	Ala	Thr	Asn	Val	Ile	Asn	Ala	Ala	Val	Ser	Val	Ile	Thr	Pro	Val					
	210					215					220									
ggc	atg	gac	cac	gtg	gat	cgc	ctg	ggc	aac	acc	att	ggt	gaa	atc	gct	720				
Gly	Met	Asp	His	Val	Asp	Arg	Leu	Gly	Asn	Thr	Ile	Gly	Glu	Ile	Ala					
225					230					235					240					
ggt	gaa	aag	gcc	ggc	atc	atc	aag	gct	cgt	cct	gca	tct	gag	gat	ggc	768				
Gly	Glu	Lys	Ala	Gly	Ile	Ile	Lys	Ala	Arg	Pro	Ala	Ser	Glu	Asp	Gly					
			245					250						255						
acc	gag	cct	gag	ggc	aac	gtt	gtc	atc	gtg	ggc	aag	cag	gag	cca	gaa	816				
Thr	Glu	Pro	Glu	Gly	Asn	Val	Val	Ile	Val	Gly	Lys	Gln	Glu	Pro	Glu					
			260					265					270							
gca	atg	aac	gtg	att	ctg	cag	caa	gcc	gtg	gac	gtg	gac	gca	gct	gtt	864				
Ala	Met	Asn	Val	Ile	Leu	Gln	Gln	Ala	Val	Asp	Val	Asp	Ala	Ala	Val					
		275					280					285								
gct	cgt	ttg	aac	atg	gaa	ttc	ggc	gtg	gtg	gaa	tcc	gcc	att	gcc	gtt	912				
Ala	Arg	Leu	Asn	Met	Glu	Phe	Gly	Val	Val	Glu	Ser	Ala	Ile	Ala	Val					
	290					295					300									
ggt	gga	cag	cag	ctc	acc	ctg	aag	ggt	ttg	ggc	ggc	gaa	tac	acc	gac	960				
Gly	Gly	Gln	Gln	Leu	Thr	Leu	Lys	Gly	Leu	Gly	Gly	Glu	Tyr	Thr	Asp					
305					310					315					320					
atc	ttc	ctc	cca	ctg	tct	ggc	gcg	cac	caa	gca	gat	aat	gcc	gcg	gtt					
1008																				
Ile	Phe	Leu	Pro	Leu	Ser	Gly	Ala	His	Gln	Ala	Asp	Asn	Ala	Ala	Val					

325	330	335
gct ctc gca gca gtg gaa gca ttt ttc ggt gca tcc gcc gga cgc cca		
1056		
Ala Leu Ala	Ala Val Glu Ala Phe Phe Gly Ala Ser Ala	Gly Arg Pro
340	345	350
ttg gat atc gac acg gtg cgc gaa ggc ttc gca caa gtt cag tcc cca		
1104		
Leu Asp Ile	Asp Thr Val Arg Glu Gly Phe Ala Gln Val	Gln Ser Pro
355	360	365
ggt cgc ctc gag cgc ctg cgc tct gca cca acc gtg ttc atc gac gca		
1152		
Gly Arg Leu	Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile	Asp Ala
370	375	380
gct cac aac cca cac ggt gcc gca gca ctt ggt gca gca cta gac cgt		
1200		
Ala His Asn	Pro His Gly Ala Ala Ala Leu Gly Ala Ala	Leu Asp Arg
385	390	395
gac ttt gag ttc cgt cgc ctc atc ggt gtc atc gga gtg ctc tgc gac		
1248		
Asp Phe Glu	Phe Arg Arg Leu Ile Gly Val Ile Gly Val	Leu Cys Asp
405	410	415
aag gat gcc cgc ggc atc ttg gaa tca ctt gag cca tac ctg cat gaa		
1296		
Lys Asp Ala	Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr	Leu His Glu
420	425	430
att gtg tgc acc cag act gcc tca gag cgc gca ttg gac gca tac gat		
1344		
Ile Val Cys	Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp	Ala Tyr Asp
435	440	445
tta gct gaa tat gct cga gag atc tac ggc gat gag cgt gtg cac gtc		
1392		
Leu Ala Glu	Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg	Val His Val
450	455	460
caa gaa gat ctt gct ggc gcg gta gaa ctc gct att gaa cta gca gaa		
1440		
Gln Glu Asp	Leu Ala Gly Ala Val Glu Leu Ala Ile Glu	Leu Ala Glu
465	470	475
gac acc gat gta cag tcc gga tca ggt gtt gtg atc acc ggt tca atc		
1488		
Asp Thr Asp	Val Gln Ser Gly Ser Gly Val Val Ile Thr	Gly Ser Ile
485	490	495
gtg acc gcc ggc gat gcg cgc acg ctg ttt gga aag gaa cct gca		
1533		
Val Thr Ala	Gly Asp Ala Arg Thr Leu Phe Gly Lys Glu	Pro Ala
500	505	510
tgagcaagcg tgaagaatca att		
1556		

<210> 698
 <211> 511
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 698

Gly Ile Gly Leu Val Ala Asn Asn Asp Gly Ile Phe Asp Ser Glu Asn
 1 5 10 15
 Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser
 20 25 30
 Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu
 35 40 45
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu
 50 55 60
 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met
 65 70 75 80
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala
 85 90 95
 Ile His Val Ala Gly Thr Asn Gly Lys Thr Ser Thr Thr Arg Met Ile
 100 105 110
 Glu Ser Leu Leu Arg Ala Phe His Arg Arg Thr Gly Arg Thr Thr Ser
 115 120 125
 Pro His Leu Gln Leu Val Thr Glu Arg Ile Ala Ile Asp Gly Lys Pro
 130 135 140
 Ile His Pro Arg Asp Phe Val Arg Ile Tyr Glu Glu Ile Lys Pro Tyr
 145 150 155 160
 Met Glu Met Thr Asp Ala Trp Ser Glu Ala Glu Gly Gly Pro Lys Met
 165 170 175
 Ser Lys Phe Glu Ala Leu Val Ala Leu Ala Tyr Ala Gly Phe Ala Asp
 180 185 190
 Ala Pro Val Asp Val Ala Val Val Glu Val Gly Leu Gly Gly Arg Trp
 195 200 205
 Asp Ala Thr Asn Val Ile Asn Ala Ala Val Ser Val Ile Thr Pro Val
 210 215 220
 Gly Met Asp His Val Asp Arg Leu Gly Asn Thr Ile Gly Glu Ile Ala
 225 230 235 240
 Gly Glu Lys Ala Gly Ile Ile Lys Ala Arg Pro Ala Ser Glu Asp Gly
 245 250 255
 Thr Glu Pro Glu Gly Asn Val Val Ile Val Gly Lys Gln Glu Pro Glu
 260 265 270
 Ala Met Asn Val Ile Leu Gln Gln Ala Val Asp Val Asp Ala Ala Val
 275 280 285
 Ala Arg Leu Asn Met Glu Phe Gly Val Val Glu Ser Ala Ile Ala Val

290	295	300
Gly Gly Gln Gln Leu Thr Leu Lys Gly Leu Gly Gly Glu Tyr Thr Asp 305 310 315 320		
Ile Phe Leu Pro Leu Ser Gly Ala His Gln Ala Asp Asn Ala Ala Val 325 330 335		
Ala Leu Ala Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro 340 345 350		
Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro 355 360 365		
Gly Arg Leu Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile Asp Ala 370 375 380		
Ala His Asn Pro His Gly Ala Ala Ala Leu Gly Ala Ala Leu Asp Arg 385 390 395 400		
Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp 405 410 415		
Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu 420 425 430		
Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp 435 440 445		
Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val 450 455 460		
Gln Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu 465 470 475 480		
Asp Thr Asp Val Gln Ser Gly Ser Gly Val Val Ile Thr Gly Ser Ile 485 490 495		
Val Thr Ala Gly Asp Ala Arg Thr Leu Phe Gly Lys Glu Pro Ala 500 505 510		

<210> 699
 <211> 600
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(577)
 <223> RXA01517

<400> 699
 tccataagcc caaagcaccg atcccacgta cttttgctga cgtcgcggtg gttgccccgac 60

gttccaggaa atccatggct gctggaagga gcaacgccta atg cat gca gtt ttg 115
 Met His Ala Val Leu
 1 5

tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg 163
 Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val

	10	15	20	
atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca				211
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser				
	25	30	35	
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg				259
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val				
	40	45	50	
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc				307
Leu Val Val Glu Val Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly				
	55	60	65	
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg				355
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly				
	70	75	80	85
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa				403
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu				
	90	95	100	
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct				451
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala				
	105	110	115	
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat				499
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp				
	120	125	130	
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat				547
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp				
	135	140	145	
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat				597
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile				
	150	155		
gca				600

<210> 700

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 700

Met	His	Ala	Val	Leu	Ser	Ile	Gly	Ser	Asn	Met	Asp	Asp	Arg	Tyr	Ala
1				5					10					15	

Leu	Leu	Asn	Thr	Val	Ile	Glu	Glu	Phe	Lys	Asp	Glu	Ile	Val	Ala	Gln
		20						25					30		

Ser	Ala	Ile	Tyr	Ser	Thr	Pro	Pro	Trp	Gly	Ile	Glu	Asp	Gln	Asp	Glu
		35					40					45			

Phe	Leu	Asn	Ala	Val	Leu	Val	Val	Glu	Val	Glu	Glu	Thr	Pro	Ile	Glu
	50					55					60				

Leu	Leu	Arg	Arg	Gly	Gln	Lys	Leu	Glu	Glu	Ala	Ala	Glu	Arg	Val	Arg
65					70					75					80

Val	Arg	Lys	Trp	Gly	Pro	Arg	Thr	Leu	Asp	Val	Asp	Ile	Val	Gln	Ile
				85					90					95	
Ile	Lys	Asp	Gly	Glu	Glu	Ile	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Thr	Leu
			100					105					110		
Pro	His	Pro	Trp	Ala	Trp	Gln	Arg	Ala	Phe	Val	Leu	Ile	Pro	Trp	Leu
		115					120					125			
Glu	Ala	Glu	Pro	Asp	Ala	Val	Leu	His	Gly	Thr	Thr	Ile	Ala	Glu	His
	130					135					140				
Val	Asp	Asn	Leu	Asp	Pro	Thr	Asp	Ile	Glu	Gly	Val	Thr	Lys	Ile	
145					150					155					

```
<210> 701
<211> 1983
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(1960)  
<223> RXA00579
```

<400> 701																
tcgtctaagt	ttttctttga	gttttcatat	gtagaaggca	tcgtcggctt	cggcctggcg	60										
gtgcttttct	cgttgttttg	tggttttgtc	agaggatgtc	atg	cgc	ggt	tta	att	115							
				Met	Arg	Val	Leu	Ile	5							
				1												
att	gat	aat	tat	gat	tct	ttc	acg	ttt	aat	ctc	gcc	acc	tat	gtg	gaa	163
Ile	Asp	Asn	Tyr	Asp	Ser	Phe	Thr	Phe	Asn	Leu	Ala	Thr	Tyr	Val	Glu	
				10				15						20		
gag	gtt	acg	ggt	cag	gca	cct	gtg	gtg	gtg	cct	aat	gat	caa	gaa	ata	211
Glu	Val	Thr	Gly	Gln	Ala	Pro	Val	Val	Val	Pro	Asn	Asp	Gln	Glu	Ile	
			25					30					35			
gat	gag	atg	ctt	ttc	gac	gcc	gtc	atc	ctc	tca	cct	ggc	ccg	ggc	cac	259
Asp	Glu	Met	Leu	Phe	Asp	Ala	Val	Ile	Leu	Ser	Pro	Gly	Pro	Gly	His	
		40					45					50				
gcc	ggc	gtt	gcg	gct	gat	ttt	ggt	atc	tgt	gca	ggc	gtc	att	gag	cgt	307
Ala	Gly	Val	Ala	Ala	Asp	Phe	Gly	Ile	Cys	Ala	Gly	Val	Ile	Glu	Arg	
	55					60				65						
gca	cgc	gtt	ccg	att	ttg	ggt	gtg	tgt	tta	ggc	cac	cag	ggc	att	gcg	355
Ala	Arg	Val	Pro	Ile	Leu	Gly	Val	Cys	Leu	Gly	His	Gln	Gly	Ile	Ala	
70					75			80							85	
ttg	gcc	tat	ggc	ggt	gat	gtt	gat	ttg	gcg	ccc	agg	ccg	gtc	cac	ggt	403
Leu	Ala	Tyr	Gly	Gly	Asp	Val	Asp	Leu	Ala	Pro	Arg	Pro	Val	His	Gly	
			90					95					100			
gag	gtt	tcg	cag	atc	acc	cat	gat	ggt	tca	ggt	tta	ttt	gca	ggc	atc	451
Glu	Val	Ser	Gln	Ile	Thr	His	Asp	Gly	Ser	Gly	Leu	Phe	Ala	Gly	Ile	
			105					110					115			

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc	499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg	
120 125 130	
ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc	547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile	
135 140 145	
atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat	595
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His	
150 155 160 165	
ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc	643
Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe	
170 175 180	
ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att	691
Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile	
185 190 195	
ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat	739
Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His	
200 205 210	
tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt	787
Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu	
215 220 225	
ggt gat gcc agc ggt cct ctc gca cgc aca aaa acc cat aat gtc ggc	835
Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly	
230 235 240 245	
gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca	883
Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser	
250 255 260	
gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt	931
Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly	
265 270 275	
tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt	979
Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser	
280 285 290	
ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa	
1027	
Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu	
295 300 305	
tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt	
1075	
Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe	
310 315 320 325	
gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct	
1123	
Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro	
330 335 340	

gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat
1171

Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr
345 350 355

ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg
1219

Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser
360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc
1267

Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala
375 380 385

cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat
1315

Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr
390 395 400 405

ggt gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg
1363

Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro
410 415 420

gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc
1411

Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro
425 430 435

att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa
1459

Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu
440 445 450

atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg
1507

Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu
455 460 465

atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc
1555

Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro
470 475 480 485

acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca
1603

Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr
490 495 500

gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt
1651

Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser
505 510 515

ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt
1699

Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly
520 525 530

gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct
1747

Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala
535 540 545

cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc
1795

Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly
550 555 560 565

gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat
1843

Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn
570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt
1983

Leu Phe Gly Val Glu Phe Pro
615 620

<210> 702

<211> 620

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 702

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu
1 5 10 15

Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro
20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser
 130 135 140
 Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp
 145 150 155 160
 Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln
 165 170 175
 Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu
 180 185 190
 Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu
 195 200 205
 Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln
 210 215 220
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys
 225 230 235 240
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp
 245 250 255
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp
 260 265 270
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala
 275 280 285
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg
 290 295 300
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu
 305 310 315 320
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val
 325 330 335
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp
 340 345 350
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile
 355 360 365
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly
 370 375 380
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala
 385 390 395 400
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile
 405 410 415
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr
 420 425 430
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala
 435 440 445
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp

450	455	460
Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala		
465	470	475 480
Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val		
	485 490	495
Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu		
	500 505	510
Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly		
	515 520	525
Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp		
	530 535	540
Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr		
	545 550	555 560
Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu		
	565 570	575
Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu		
	580 585	590
Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser		
	595 600	605
Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro		
	610 615	620

<210> 703

<211> 747

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(724)

<223> RXA00958

<400> 703

attctaattcc tcaatctgaa gccgatgaga cgttgcacaa ggcgtatgcc gtgttgaatg 60

ccattgcgct tgctgctggt tccactttgg aggtcatccg atg aca cac gtt gtt 115
 Met Thr His Val Val
 1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
 Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
 10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
 Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
 25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
 Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
 40 45 50


```

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
  55                60                65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
  70                75                80                85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
                90                95                100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451
Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
                105                110                115

gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
                120                125                130

cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
                135                140                145

gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
                150                155                160                165

ggg gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
                170                175                180

ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
                185                190                195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744
Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
                200                205

tca 747

```

<210> 704

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 704

```

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn
  1                5                10                15

```

```

Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
                20                25                30

```

```

Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile
                35                40                45

```

```

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
  50                55                60

```

Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro L u Leu Gly Il Cys
 65 70 75 80
 Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro
 85 90 95
 Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
 100 105 110
 Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
 115 120 125
 Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His
 130 135 140
 Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr
 145 150 155 160
 Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp
 165 170 175
 Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro
 180 185 190
 Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
 195 200 205

<210> 705
 <211> 1266
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1243)
 <223> RXA02790

<400> 705
 tggatgctcg caccgagcc cttgaaccac aatccacaga caccgaagat ttcgacgaga 60
 agggaaattt cccaggatga accaaatccg aaaccgccgg atg gag ccc gtc tac 115
 Met Glu Pro Val Tyr
 1 5
 gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
 Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
 10 15 20
 ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211
 Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
 25 30 35
 acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259
 Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
 40 45 50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu 55 60 65	307
gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser 70 75 80 85	355
aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln 90 95 100	403
gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp 105 110 115	451
aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp 120 125 130	499
gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile 135 140 145	547
gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu 150 155 160 165	595
gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val 170 175 180	643
cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys 185 190 195	691
cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser 200 205 210	739
aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn 215 220 225	787
cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu 230 235 240 245	835
act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala 250 255 260	883
cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu 265 270 275	931
gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu 280 285 290	979

tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc
1027
Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr
295 300 305

cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc
1075
Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala
310 315 320 325

gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga
1123
Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly
330 335 340

aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc
1171
Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe
345 350 355

aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac
1219
Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn
360 365 370

agt ggc gtt cta gac agc aac cga taaggatcag cgaataaaat tgg
1266
Ser Gly Val Leu Asp Ser Asn Arg
375 380

<210> 706

<211> 381

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 706

Met Glu Pro Val Tyr Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr
1 5 10 15

Ile Ala Ser Leu Ile Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val
20 25 30

Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly
35 40 45

Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu
50 55 60

Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe
65 70 75 80

Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly
85 90 95

Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala
100 105 110

Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly
115 120 125

Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly
 130 135 140
 Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn
 145 150 155 160
 Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro
 165 170 175
 Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg
 180 185 190
 Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr
 195 200 205
 Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile
 210 215 220
 Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala
 225 230 235 240
 Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu
 245 250 255
 Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val
 260 265 270
 Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr
 275 280 285
 Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp
 290 295 300
 Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro
 305 310 315 320
 Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu
 325 330 335
 Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
 340 345 350
 Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile
 355 360 365
 Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg
 370 375 380

<210> 707

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 707

tggagctcaa caaggcagcg tacatgtttg agtacagctt cgatgacatc accgtgtccg 60

gctacgatcc acacccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115
Met Ile Gly Ala Ile
1 5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
70 75 80 85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
135 140 145

atc aag gtt taaggagcaa acaacatgag caa 579
Ile Lys Val
150

<210> 708

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 708

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
1 5 10 15

Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
20 25 30

Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
35 40 45

Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
50 55 60

Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
65 70 75 80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
85 90 95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
100 105 110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
115 120 125

Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
130 135 140

Lys Phe Gln Arg Tyr Ile Lys Val
145 150

<210> 709

<211> 2599

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2599)

<223> RXN02198

<400> 709

agactagtgg cgctttgcct gtgttgctta ggcggcgcttg aaaatgaact acgaatgaaa 60

agttcgggaa ttgtctaatac cgtactaagc tgtctacaca atg tct act tca gtt 115
Met Ser Thr Ser Val
1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
40 45 50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
55 60 65

cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg

				90				95				100							
tgc	cgt	gag	ctt	gcc	tac	aag	ggc	act	gca	gtg	gct	agg	gaa	gtg	gct	451			
Cys	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	Thr	Ala	Val	Ala	Arg	Glu	Val	Ala				
105				110				115											
gat	gag	atg	ggg	ccg	ggc	cga	aac	ggc	atg	cgg	cgt	ttc	gtg	gtt	ggg	499			
Asp	Glu	Met	Gly	Pro	Gly	Arg	Asn	Gly	Met	Arg	Arg	Phe	Val	Val	Gly				
120				125				130											
tcc	ctg	gga	cct	gga	acg	aag	ctt	cca	tcg	ctg	ggc	cat	gca	ccg	tat	547			
Ser	Leu	Gly	Pro	Gly	Thr	Lys	Leu	Pro	Ser	Leu	Gly	His	Ala	Pro	Tyr				
135				140				145											
gca	gat	ttg	cgt	ggg	cac	tac	aag	gaa	gca	gcg	ctt	ggc	atc	atc	gac	595			
Ala	Asp	Leu	Arg	Gly	His	Tyr	Lys	Glu	Ala	Ala	Leu	Gly	Ile	Ile	Asp				
150				155				160				165							
ggg	ggg	ggc	gat	gcc	ttt	ttg	att	gag	act	gct	cag	gac	ttg	ctt	cag	643			
Gly	Gly	Gly	Asp	Ala	Phe	Leu	Ile	Glu	Thr	Ala	Gln	Asp	Leu	Leu	Gln				
170				175				180											
gtc	aag	gct	gcg	gtt	cac	ggc	gtt	caa	gat	gcc	atg	gct	gaa	ctt	gat	691			
Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala	Met	Ala	Glu	Leu	Asp				
185				190				195											
aca	ttc	ttg	ccc	att	att	tgc	cac	gtc	acc	gta	gag	acc	acc	ggc	acc	739			
Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val	Glu	Thr	Thr	Gly	Thr				
200				205				210											
atg	ctc	atg	ggg	tct	gag	atc	ggg	gcc	gcg	ttg	aca	gcg	ctg	cag	cca	787			
Met	Leu	Met	Gly	Ser	Glu	Ile	Gly	Ala	Ala	Leu	Thr	Ala	Leu	Gln	Pro				
215				220				225											
ctg	ggg	atc	gac	atg	att	ggg	ctg	aac	tgc	gcc	acc	ggc	cca	gat	gag	835			
Leu	Gly	Ile	Asp	Met	Ile	Gly	Leu	Asn	Cys	Ala	Thr	Gly	Pro	Asp	Glu				
230				235				240				245							
atg	agc	gag	cac	ctg	cgt	tac	ctg	tcc	aag	cac	gcc	gat	att	cct	gtg	883			
Met	Ser	Glu	His	Leu	Arg	Tyr	Leu	Ser	Lys	His	Ala	Asp	Ile	Pro	Val				
250				255				260											
tcg	gtg	atg	cct	aac	gca	ggg	ctt	cct	gtc	ctg	ggg	aaa	aac	ggg	gca	931			
Ser	Val	Met	Pro	Asn	Ala	Gly	Leu	Pro	Val	Leu	Gly	Lys	Asn	Gly	Ala				
265				270				275											
gaa	tac	cca	ctt	gag	gct	gag	gat	ttg	gcg	cag	gcg	ctg	gct	gga	ttc	979			
Glu	Tyr	Pro	Leu	Glu	Ala	Glu	Asp	Leu	Ala	Gln	Ala	Leu	Ala	Gly	Phe				
280				285				290											
gtc	tcc	gaa	tat	ggc	ctg	tcc	atg	gtg	ggg	ggg	tgt	tgt	ggc	acc	aca	1027			
Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly	Cys	Cys	Gly	Thr	Thr				
295				300				305											
cct	gag	cac	atc	cgt	gcg	gtc	cgc	gat	gcg	gtg	gtt	ggg	gtt	cca	gag	1075			
Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val									

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag
1123
Gln Glu Thr S r Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc
1171
Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc
1219
Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc
1267
Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt
1315
Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc
1363
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg
1411
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu
425 430 435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt
1459
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu
440 445 450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac
1507
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
455 460 465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag
1555
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag
1603
Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac
1651
Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac
1699
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp
520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat
1747
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca
1795
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac
1843
Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
570 575 580

cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att
1891
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile
585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg
1939
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
600 605 610

atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc
1987
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
615 620 625

tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag
2035
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
630 635 640 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa
2083
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu
650 655 660

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc
2131
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag
2179
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
680 685 690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg
2227
Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc
 2275
 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
 710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa
 2323
 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
 730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag
 2371
 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
 745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat
 2419
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
 760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac
 2467
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
 775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca
 2515
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
 790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg
 2563
 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
 810 815 820

aag tcc acc gtg gtg atg aag caa acc atc agc gac
 2599
 Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser Asp
 825 830

<210> 710

<211> 833

<212> PRT

<213> Corynebacterium glutamicum

<400> 710

Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser
 1 5 10 15

Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala
 20 25 30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
 35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
 50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
 65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
 85 90 95
 Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
 100 105 110
 Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
 115 120 125
 Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
 130 135 140
 Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
 145 150 155 160
 Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
 165 170 175
 Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
 180 185 190
 Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
 195 200 205
 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
 210 215 220
 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
 225 230 235 240
 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
 245 250 255
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
 260 265 270
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
 275 280 285
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
 290 295 300
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
 305 310 315 320
 Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala
 325 330 335
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val
 340 345 350
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
 355 360 365
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
 370 375 380
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln
 385 390 395 400

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
 660 665 670
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
 675 680 685
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
 705 710 715 720
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala

	725		730		735
Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly	740		745		750
Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys	755		760		765
Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser	770		775		780
Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser	785		790		795
Ala Met Leu Glu Ala Ala Glu Glu His Lys Ala Asp Val Ile Gly Met	805		810		815
Ser Gly Leu Leu Val Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser	820		825		830

Asp

<210> 711
 <211> 2578
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2578)
 <223> FRXA02198

<400> 711
 agactagtgg cgctttgcct gtgttgctta ggcggcgcttg aaaatgaact acgaatgaaa 60
 agttcgggaa ttgtctaata cgtactaagc tgtctacaca atg tct act tca gtt 115
 Met Ser Thr Ser Val
 1 5
 act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20
 ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
 25 30 35
 caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
 Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
 40 45 50
 tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
 55 60 65
 cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt	403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg	
90 95 100	
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct	451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala	
105 110 115	
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt	499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly	
120 125 130	
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat	547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	
135 140 145	
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac	595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp	
150 155 160 165	
ggg ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag	643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln	
170 175 180	
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat	691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
185 190 195	
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc	739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
200 205 210	
atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca	787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
215 220 225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag	835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
230 235 240 245	
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg	883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	
250 255 260	
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca	931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	
265 270 275	
gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc	979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe	
280 285 290	
gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca	
1027	
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
295 300 305	
cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag	
1075	
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	
310 315 320 325	

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag
1123

Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc
1171

Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc
1219

Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc
1267

Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt
1315

Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc
1363

Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg
1411

Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu
425 430 435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt
1459

Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu
440 445 450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac
1507

Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
455 460 465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag
1555

Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag
1603

Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac
1651

Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac
1699
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp
520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat
1747
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca
1795
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac
1843
Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
570 575 580

cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att
1891
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile
585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg
1939
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
600 605 610

atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc
1987
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
615 620 625

tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag
2035
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
630 635 640 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa
2083
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu
650 655 660

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc
2131
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag
2179
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
680 685 690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg
2227
Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc
 2275
 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
 710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa
 2323
 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
 730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag
 2371
 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
 745 750 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat
 2419
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
 760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac
 2467
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
 775 780 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca
 2515
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
 790 795 800 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg
 2563
 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
 810 815 820

aag tcc acc gtg gtg
 2578
 Lys Ser Thr Val Val
 825

<210> 712
 <211> 826
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 712
 Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser
 1 5 10 15

Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala
 20 25 30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
 35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
 50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
 65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
 85 90 95
 Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
 100 105 110
 Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
 115 120 125
 Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
 130 135 140
 Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
 145 150 155 160
 Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
 165 170 175
 Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
 180 185 190
 Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
 195 200 205
 Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
 210 215 220
 Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
 225 230 235 240
 Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
 245 250 255
 Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
 260 265 270
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
 275 280 285
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
 290 295 300
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
 305 310 315 320
 Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala
 325 330 335
 Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val
 340 345 350
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
 355 360 365
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
 370 375 380
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln
 385 390 395 400

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
 660 665 670
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
 675 680 685
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
 705 710 715 720
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala

725								730				735			
Val	Ala	Tyr	Leu	Glu	Pro	Phe	Met	Glu	Glu	Glu	Ala	Glu	Ala	Thr	Gly
740								745				750			
Ser	Ala	Gln	Ala	Glu	Gly	Lys	Gly	Lys	Ile	Val	Val	Ala	Thr	Val	Lys
755								760				765			
Gly	Asp	Val	His	Asp	Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser
770								775				780			
Asn	Asn	Gly	Tyr	Asp	Val	Val	Asn	Leu	Gly	Ile	Lys	Gln	Pro	Leu	Ser
785								790				795			
Ala	Met	Leu	Glu	Ala	Ala	Glu	Glu	His	Lys	Ala	Asp	Val	Ile	Gly	Met
805								810				815			
Ser	Gly	Leu	Leu	Val	Lys	Ser	Thr	Val	Val						
820								825							

```
<210> 713
<211> 2358
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(2335)  
<223> RXN02085
```

<400> 713																	
caccgcgtga tttcgcgaac cttgaaacat cgtcagaaga ttgccgtgcg tcctagccgg																	60
gatccgcacg ttcgggtcaa gcagaaagtc tttaactcac																	
											atg	act	tcc	aac	ttt		115
											Met	Thr	Ser	Asn	Phe		
											1				5		
tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg																	163
Ser	Ser	Thr	Val	Ala	Gly	Leu	Pro	Arg	Ile	Gly	Ala	Lys	Arg	Glu	Leu		
				10				15						20			
aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa																	211
Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu		
			25					30					35				
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg																	259
Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr	Ala	Ser	Asp	Ser	Leu		
		40				45						50					
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca																	307
Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg	Ser	Tyr	Tyr	Asp	Ala		
	55					60					65						
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat																	355
Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu	Pro	Glu	Arg	Phe	Asp		
	70				75					80					85		
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc																	403
Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro	Leu	Trp	Ile	Asp	Arg		
				90				95						100			

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
105 110 115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
120 125 130	
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
135 140 145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt	595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
150 155 160 165	
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
170 175 180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
250 255 260	
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc	
1027	
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
295 300 305	
ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac	
1075	
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	
acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc	
1123	

Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340
 ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355
 gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
 1219
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370
 gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385
 cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405
 aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
 1363
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420
 cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
 1411
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435
 tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450
 ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
 1507
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
 455 460 465
 ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc
 1555
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
 470 475 480 485
 gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc
 1603
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
 490 495 500
 cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
 1651
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
 505 510 515
 cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys

520	525	530
cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc 1747		
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser 535 540 545		
ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca 1795		
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala 550 555 560 565		
ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag 1843		
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys 570 575 580		
atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga 1891		
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg 585 590 595		
gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc 1939		
Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg 600 605 610		
ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg 1987		
Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met 615 620 625		
tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat 2035		
Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp 630 635 640 645		
gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc 2083		
Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu 650 655 660		
gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg 2131		
Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val 665 670 675		
tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt 2179		
Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly 680 685 690		
ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc 2227		
Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val 695 700 705		
aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct 2275		
Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala 710 715 720 725		

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc
2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
730 735 740

gga gca act atc taaattgggt taccgctagg aac
2358

Gly Ala Thr Ile
745

<210> 714

<211> 745

<212> PRT

<213> Corynebacterium glutamicum

<400> 714

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
210 215 220

Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr

225		230		235		240
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly	245		250		255	
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu	260		265		270	
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly	275		280		285	
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys	290		295		300	
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu	305		310		315	320
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val	325		330		335	
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu	340		345		350	
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala	355		360		365	
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro	370		375		380	
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg	385		390		395	400
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr	405		410		415	
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala	420		425		430	
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met	435		440		445	
Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu	450		455		460	
Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr	465		470		475	480
Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val	485		490		495	
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn	500		505		510	
Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln	515		520		525	
Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr	530		535		540	
Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr	545		550		555	560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
565 570 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
580 585 590

Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
595 600 605

Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
610 615 620

Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
625 630 635 640

Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
645 650 655

Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
660 665 670

Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
675 680 685

Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
690 695 700

Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
705 710 715 720

Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln
725 730 735

Ala Arg Glu Lys Ile Gly Ala Thr Ile
740 745

<210> 715

<211> 1923

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1900)

<223> FRXA02085

<400> 715

caccggtga ttctgcgaac cttgaaacat cgtcagaaga ttgccgtgcg tcctagccgg 60

gatccgcacg ttccggtcaa gcagaaagtc tttaactcac atg act tcc aac ttt 115
Met Thr Ser Asn Phe
1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
10 15 20

aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu

25	30	35	
ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu			259
40	45	50	
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala			307
55	60	65	
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp			355
70	75	80	85
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg			403
	90	95	100
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met			451
	105	110	115
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser			499
	120	125	130
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu			547
	135	140	145
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly			595
	150	155	160
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro			643
	170	175	180
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys			691
	185	190	195
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr			739
	200	205	210
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr			787
	215	220	225
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly			835
	230	235	240
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly			883
	250	255	260
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly			931
	265	270	275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc
 1027
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac
 1075
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
 1123
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
 1219
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
 1363
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
 1411
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
 1507
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
 455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc
1555

Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc
1603

Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
1651

Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
1699

Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc
1747

His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca
1795

Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag
1843

Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg
1891

Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
585 590 595

aga cgt cga taagcctgcc tacctgcagt ggt
1923

Arg Arg Arg
600

<210> 716

<211> 600

<212> PRT

<213> Corynebacterium glutamicum

<400> 716

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro

370						375						380					
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg																	
385					390					395							400
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr																	
				405						410							415
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala																	
			420						425						430		
Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met																	
			435						440					445			
Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu																	
			450						455					460			
Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr																	
									470					475			480
Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val																	
														490			495
Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn																	
			500						505								510
Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln																	
			515						520								525
Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr																	
			530						535					540			
Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr																	
														555			560
Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile																	
														570			575
Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu																	
			580						585								590
Leu Leu Pro Ala Thr Arg Arg Arg																	
			595						600								

<210> 717
 <211> 603
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(580)
 <223> FRXA02086

<400> 717
 gatgatcagc cgctggctac cactgctgac caggttgac tggcactgcg cgatgaaatt 60
 aacgatctca tcgaggctgg cgccaagatc atccaggtgg atg agc ctg cga ttc 115
 Met Ser Leu Arg Phe
 1 5

gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
10 15 20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
25 30 35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc^o aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
40 45 50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
55 60 65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
70 75 80 85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
90 95 100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
105 110 115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
120 125 130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
135 140 145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
150 155 160

aac 603

<210> 718

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 718

Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
1 5 10 15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
20 25 30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
35 40 45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
50 55 60

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
 115 120 125
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
 130 135 140
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
 145 150 155 160

<210> 719
 <211> 1326
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1303)
 <223> RXN02648

<400> 719
 atgaataaaaa ttccgggtgc agtgaccgta ggtgaggttaa acgcggttag agtcgaatga 60
 gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115
 Met Ser Gln Asn Arg
 1 5
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403

Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg	Trp	Ala	Ser	Gln	Glu		
				90					95					100			
gca	gtg	cgt	tcc	acc	cct	ggc	aac	atc	gag	ctg	acc	agc	ttc	tct	gat	451	
Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu	Thr	Ser	Phe	Ser	Asp		
			105				110						115				
cgt	cgc	gac	cgc	gca	ttg	ttc	agc	gaa	gca	tac	gag	gat	cca	gta	tct	499	
Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr	Glu	Asp	Pro	Val	Ser		
		120					125					130					
ggc	atc	ttc	acc	ggg	cgc	gct	tct	gtg	ggc	aac	cca	gag	ttc	acc	gga	547	
Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn	Pro	Glu	Phe	Thr	Gly		
	135					140					145						
cct	att	acc	tac	att	ggc	cag	gaa	gaa	act	cag	acg	gat	gtt	gat	ctg	595	
Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Val	Asp	Leu		
150					155					160					165		
ctg	aag	aag	ggc	atg	aac	gca	gcg	gga	gct	acc	gac	ggc	ttc	gtt	gca	643	
Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala		
				170				175						180			
gca	cta	tcc	cca	gga	tct	gca	gct	cga	ttg	acc	aac	aag	ttc	tac	gac	691	
Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp		
			185					190					195				
act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gcg	ctt	tcc	cag	gaa	739	
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu		
		200					205					210					
tac	aag	atc	atc	acc	gat	gca	ggg	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787	
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro		
	215					220					225						
gac	ttg	gca	gaa	gca	tgg	gat	cag	atc	aac	cca	gag	cca	agc	gtg	aag	835	
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys		
230					235					240					245		
gat	tac	ttg	gac	tgg	atc	ggg	aca	cgc	atc	gat	gcc	atc	aac	agt	gca	883	
Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp	Ala	Ile	Asn	Ser	Ala		
				250					255					260			
gtg	aag	ggc	ctt	cca	aag	gaa	cag	acc	cgc	ctg	cac	atc	tgc	tgg	ggc	931	
Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile	Cys	Trp	Gly		
			265					270					275				
tct	tgg	cac	gga	cca	cac	gtc	act	gac	atc	cca	ttc	ggg	gac	atc	att	979	
Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly	Asp	Ile	Ile		
		280					285					290					
ggg	gag	atc	ctg	cgc	gca	gag	gtc	ggg	ggc	ttc	tcc	ttc	gaa	ggc	gca		
1027																	
Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe	Glu	Gly	Ala		
	295					300					305						
tct	cct	cgt	cac	gca	cac	gag	tgg	cgt	gta	tgg	gaa	gaa	aac	aag	ctt		
1075																	
Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu	Asn	Lys	Leu		
310					315					320					325		

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac
1123

Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc
1171

Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg
1219

Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta
1267

Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac
1313

Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
390 395 400

aacgagggtt gct
1326

<210> 720

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 720

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400

Phe

<210> 721
 <211> 548
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1) .. (525)

<223> FRXA02648

<400> 721

```

gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca 48
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1           5           10           15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
          20           25           30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
          35           40           45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
          50           55           60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
        65           70           75           80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
          85           90           95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
          100           105           110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
          115           120           125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
          130           135           140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
          145           150           155           160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
          165           170           175

taagctagac aacgagggtt gct 548

```

<210> 722

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 722

```

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1           5           10           15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
          20           25           30

```

Asn	Ser	Ala	Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile
		35					40					45			
Cys	Trp	Gly	Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly
	50					55					60				
Asp	Ile	Ile	Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe
65					70					75					80
Glu	Gly	Ala	Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu
				85					90					95	
Asn	Lys	Leu	Pro	Glu	Gly	Ser	Val	Ile	Tyr	Pro	Gly	Val	Val	Ser	His
			100					105					110		
Ser	Ile	Asn	Ala	Val	Glu	His	Pro	Arg	Leu	Val	Ala	Asp	Arg	Ile	Val
		115					120					125			
Gln	Phe	Ala	Lys	Leu	Val	Gly	Pro	Glu	Asn	Val	Ile	Ala	Ser	Thr	Asp
	130					135					140				
Cys	Gly	Leu	Gly	Gly	Arg	Leu	His	Ser	Gln	Ile	Ala	Trp	Ala	Lys	Leu
145					150					155					160
Glu	Ser	Leu	Val	Glu	Gly	Ala	Arg	Ile	Ala	Ser	Lys	Glu	Leu	Phe	
				165					170					175	

```
<210> 723
<211> 784
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(784)  
<223> FRXA02658
```

<400> 723																	
atgaataaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcgggttag agtcgaatga																	60
gagtttgata ctttcttttcg acttttagat tggattttca																	
											atg	agc	cag	aac	cgc		115
											Met	Ser	Gln	Asn	Arg		
											1				5		
atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt																	163
Ile	Arg	Thr	Thr	His	Val	Gly	Ser	Leu	Pro	Arg	Thr	Pro	Glu	Leu	Leu		
				10					15					20			
gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc																	211
Asp	Ala	Asn	Ile	Lys	Arg	Ser	Asn	Gly	Glu	Ile	Gly	Glu	Glu	Glu	Phe		
			25					30					35				
ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt																	259
Phe	Gln	Ile	Leu	Gln	Ser	Ser	Val	Asp	Asp	Val	Ile	Lys	Arg	Gln	Val		
		40					45					50					
gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc																	307
Asp	Leu	Gly	Ile	Asp	Ile	Leu	Asn	Glu	Gly	Glu	Tyr	Gly	His	Val	Thr		
	55					60					65						

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100
 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145
 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165
 ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180
 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195
 act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210
 tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 724

<211> 228

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 724

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15
 Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn

[illegible]

```
<210> 725
<211> 551
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (1)..(528)  
<223> RXS02197
```

<400> 725																
gcc	gaa	cgc	atg	cgc	ttt	agc	ttc	cca	cgc	cag	cag	cgc	ggc	agg	ttc	48
Ala	Glu	Arg	Met	Arg	Phe	Ser	Phe	Pro	Arg	Gln	Gln	Arg	Gly	Arg	Phe	
1				5					10					15		
ttg	tgc	atc	gcg	gat	ttc	att	cgc	cca	cgc	gag	caa	gct	gtc	aag	gac	96
Leu	Cys	Ile	Ala	Asp	Phe	Ile	Arg	Pro	Arg	Glu	Gln	Ala	Val	Lys	Asp	
			20					25					30			
ggc	caa	gtg	gac	gtc	atg	cca	ttc	cag	ctg	gtc	acc	atg	ggg	aat	cct	144
Gly	Gln	Val	Asp	Val	Met	Pro	Phe	Gln	Leu	Val	Thr	Met	Gly	Asn	Pro	
		35					40					45				
att	gct	gat	ttc	gcc	aac	gag	ttg	ttc	gca	gcc	aat	gaa	tac	cgc	gag	192
Ile	Ala	Asp	Phe	Ala	Asn	Glu	Leu	Phe	Ala	Ala	Asn	Glu	Tyr	Arg	Glu	
	50					55					60					
tac	ttg	gaa	gtt	cac	ggc	atc	ggc	gtg	cag	ctc	acc	gaa	gca	ttg	gcc	240

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80
 gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt 288
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95
 gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110
 ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125
 gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt 432
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140
 atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc 480
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160
 aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc 528
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175
 taacaccttt gagagggaaa act 551

<210> 726

<211> 176

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 726

Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
 1 5 10 15
 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
 20 25 30
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
 35 40 45
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg

130	135	140
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser		
145	150	155 160
Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val		
165	170	175

<210> 727
 <211> 546
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(523)
 <223> RXC00988

<400> 727
 tagcagaaga caccgatgta cagtccggat caggtgttgt gatcaccggt tcaatcgtga 60

ccgccggcga tgcgcgcacg ctgtttggaa aggaacctgc atg agc aag cgt gaa 115
 Met Ser Lys Arg Glu
 1 5

gaa tca att gag tac gga cca tta ggc aaa ggc cac gat cca tta aag 163
 Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys
 10 15 20

gat ccc atg aag ggt atc cga ggt gtc atg gcc ggc acc tta gtg atg 211
 Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met
 25 30 35

gaa gca atc acc tta ggt ctt gtt ctc acc gtg att ctg cgc gtg gac 259
 Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp
 40 45 50

gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc 307
 Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val Tyr Val Ser Ala Val
 55 60 65

gcg atc gca cac ttt gtt gct gca ttt ctg caa agg ttt agt tgg tcc 355
 Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln Arg Phe Ser Trp Ser
 70 75 80 85

atc ccg atg aac atc gtg ctg cag gtt ctt gca ctt gcc ggt ttc ttt 403
 Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe
 90 95 100

gtt cac ccc gcg atg ggc ttc gcc gcc atc atc ttc atc atc gcg tgg 451
 Val His Pro Ala Met Gly Phe Ala Ala Ile Ile Phe Ile Ile Ala Trp
 105 110 115

gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc 499
 Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg
 120 125 130

ggg ctg ctt acc acg cag cac agc taagctttaa ggcctccgg ggc 546
 Gly Leu Leu Thr Thr Gln His Ser
 135 140

<210> 728
 <211> 141
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 728
 Met Ser Lys Arg Glu Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly
 1 5 10 15
 His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala
 20 25 30
 Gly Thr Leu Val Met Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val
 35 40 45
 Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val
 50 55 60
 Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln
 65 70 75 80
 Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala
 85 90 95
 Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile
 100 105 110
 Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile
 115 120 125
 Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser
 130 135 140

<210> 729
 <211> 597
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(574)
 <223> RXC01518

<400> 729
 agcagaacct gatgccgtcc tgcacggcac gaccattgca gaacatgtgg ataattcttga 60
 tcccacagac attgaagggtg tcaccaagat ttaaggagtc gtg gct ttc atg cag 115
 Val Ala Phe Met Gln
 1 5
 aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
 Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
 10 15 20
 gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211

Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
 25 30 35
 tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259
 Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly
 40 45 50
 ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc 307
 Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly
 55 60 65
 cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg 355
 Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met
 70 75 80 85
 ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat 403
 Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr
 90 95 100
 gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451
 Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala
 105 110 115
 gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc 499
 Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile
 120 125 130
 gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547
 Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro
 135 140 145
 cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcattgaatc 594
 Pro Pro Gln Ser Gly Glu Ala Ile Ser
 150 155
 aag 597

<210> 730

<211> 158

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 730

Val Ala Phe Met Gln Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly
 1 5 10 15
 Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly
 20 25 30
 Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu
 35 40 45
 Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp
 50 55 60
 Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile
 65 70 75 80
 Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile
 85 90 95

Phe	Gly	Gly	Val	Tyr	Val	Gly	Ile	Gly	Ser	Tyr	Val	Ile	Pro	Arg	Ala	
			100							105				110		
Gly	Glu	Leu	Ser	Ala	Ala	Ser	Asn	Asp	Leu	Pro	Gly	Val	Ile	Ala	Cys	
			115							120				125		
Ala	Leu	Gly	Gly	Ile	Ala	Leu	Ser	Ala	Ala	Gly	Leu	Tyr	Leu	Glu	Arg	
		130						135						140		
Ser	Cys	Glu	Ala	Pro	Pro	Pro	Gln	Ser	Gly	Glu	Ala	Ile	Ser			
		145												150		
																155

```
<210> 731
<211> 723
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101) .. (700)  
<223> RXC01942
```

<400> 731																
gccgcgaaat	tcggtgaaat	tgaaggtatt	cctgcagatc	aggcaaattc	ttccacgact	60										
gtgatcaagg	tcaacggcaa	gaacgagtaa	cctgggatcc	atg	ttg	cgc	att	gga	115							
				Met	Leu	Arg	Ile	Gly	5							
				1												
cta	aca	gga	ggg	atc	ggc	agc	ggt	aaa	tct	acc	gtt	gcc	gat	ctt	ttg	163
Leu	Thr	Gly	Gly	Ile	Gly	Ser	Gly	Lys	Ser	Thr	Val	Ala	Asp	Leu	Leu	
				10				15						20		
tca	tct	gaa	gga	ttt	ctc	atc	gtc	gac	gcg	gac	caa	gtt	gcc	cgc	gat	211
Ser	Ser	Glu	Gly	Phe	Leu	Ile	Val	Asp	Ala	Asp	Gln	Val	Ala	Arg	Asp	
			25					30					35			
atc	gtc	gaa	ccc	gga	caa	ccg	gca	tta	gca	gag	cta	gct	gaa	gct	ttt	259
Ile	Val	Glu	Pro	Gly	Gln	Pro	Ala	Leu	Ala	Glu	Leu	Ala	Glu	Ala	Phe	
		40					45					50				
ggc	caa	gac	atc	tta	aaa	ccc	gac	ggc	act	cta	gac	cgc	gcg	gga	tta	307
Gly	Gln	Asp	Ile	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Asp	Arg	Ala	Gly	Leu	
	55					60					65					
gca	gcc	aaa	gca	ttt	gtc	agc	gaa	gaa	caa	aca	gcg	ctg	ctc	aat	gcc	355
Ala	Ala	Lys	Ala	Phe	Val	Ser	Glu	Glu	Gln	Thr	Ala	Leu	Leu	Asn	Ala	
	70				75				80						85	
att	acc	cac	cct	cgt	atc	gcc	gaa	gag	tca	gct	cgt	cga	ttc	aac	gaa	403
Ile	Thr	His	Pro	Arg	Ile	Ala	Glu	Glu	Ser	Ala	Arg	Arg	Phe	Asn	Glu	
				90					95					100		
gcc	gaa	gat	caa	ggc	gcc	aaa	gtt	gcg	gtt	tat	gac	atg	cct	ttg	ctt	451
Ala	Glu	Asp	Gln	Gly	Ala	Lys	Val	Ala	Val	Tyr	Asp	Met	Pro	Leu	Leu	
			105					110					115			
gta	gaa	aaa	ggc	ctt	gac	cgc	aag	atg	gac	ctt	gtc	gtc	gta	gtt	gat	499
Val	Glu	Lys	Gly	Leu	Asp	Arg	Lys	Met	Asp	Leu	Val	Val	Val	Val	Asp	

120	125	130	
gtt gac gta gag gaa cgc gtc cgc aga ctt gtg gaa aaa cgt ggc ctc			547
Val Asp Val Glu Glu Arg Val Arg Arg Leu Val Glu Lys Arg Gly Leu			
135	140	145	
aca gag gac gac gtg cgg cgt cga atc gct tct caa gtg ccc gac gac			595
Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp			
150	155	160	165
gtc aga ctt aaa gcc gct gac atc gtt gtg gac aat aac ggc acg cta			643
Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu			
	170	175	180
gag gac ctt cat gct gaa gca agc aag ctg att gct gag att ctt agt			691
Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile Ala Glu Ile Leu Ser			
	185	190	195
cgc gtg aat tagcactaaa acatcgtcaa agt			723
Arg Val Asn			
200			

<210> 732

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 732

Met Leu Arg Ile Gly Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr			
1	5	10	15
Val Ala Asp Leu Leu Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp			
	20	25	30
Gln Val Ala Arg Asp Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu			
	35	40	45
Leu Ala Glu Ala Phe Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu			
	50	55	60
Asp Arg Ala Gly Leu Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr			
	65	70	75
Ala Leu Leu Asn Ala Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala			
	85	90	95
Arg Arg Phe Asn Glu Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr			
	100	105	110
Asp Met Pro Leu Leu Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu			
	115	120	125
Val Val Val Val Asp Val Asp Val Glu Glu Arg Val Arg Arg Leu Val			
	130	135	140
Glu Lys Arg Gly Leu Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser			
	145	150	155
Gln Val Pro Asp Asp Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp			
	165	170	175

Asn Asn Gly Thr Leu Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile
 180 185 190

Ala Glu Ile Leu Ser Arg Val Asn
 195 200

<210> 733

<211> 1194

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1171)

<223> RXN02802

<400> 733

ccttcgccgc ctgctccgac ctcgccgacg ccgtcaaagc ccagggtccc atctggaaag 60

agcaaacgcg cctcgacggc tccaccgatt gggtcggcct gtg aaa aac ctc gac 115
 Val Lys Asn Leu Asp
 1 5

atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163
 Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln
 10 15 20

aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211
 Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly
 25 30 35

ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259
 Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly
 40 45 50

cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307
 His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His
 55 60 65

cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355
 Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu
 70 75 80 85

tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403
 Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr
 90 95 100

gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451
 Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala
 105 110 115

gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
 120 125 130

ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc cac gtc tgg gca 547
 Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro His Val Trp Ala
 135 140 145

tcc atc ctg ggt ttc gac gcc caa ctc tcc gtc ttc cac gcc ggc cac 595
 Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val Phe His Ala Gly His
 150 155 160 165

ggc ccc atc tac gaa gac ctc ttc ccc acc ccg cca cca ccc gga tcc 643
 Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro Pro Pro Pro Gly Ser
 170 175 180

gtc cca tca tgt tcc caa gca ggc gtt ttg ggt cca gtt gtc ggc gta 691
 Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly Pro Val Val Gly Val
 185 190 195

atg ggc tcc gcg atg gcc atg gaa gcc ctg aaa atc atc acc ggc gtg 739
 Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val
 200 205 210

ggc aca ccc ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc 787
 Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly
 215 220 225

acc tgg gaa tac atc ccc gtc gtc ggt tgc ccg gag gtg ctg gaa cgg 835
 Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg
 230 235 240 245

gtg ctt ggg tct gct ggt gtt tgc ggg att tct ggc ggt ttt ggt gag 883
 Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu
 250 255 260

gtg ctc gat gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tgc ctc 931
 Val Leu Asp Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu
 265 270 275

atc gac gtc cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc 979
 Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly
 280 285 290

gcg cac aac acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc
 1027
 Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro
 295 300 305

tcc gtt tcc gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc
 1075
 Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val
 310 315 320 325

cgc tcc gca caa gcc atc gca att tta gaa tcc gca ggc tac acc gga
 1123
 Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly
 330 335 340

atg agc agc ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg
 1171
 Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
 345 350 355

taaaaccaag gcgttggtgcc acc
 1194

<210> 734

<211> 357

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 734

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
 1 5 10 15
 Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
 20 25 30
 Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
 35 40 45
 Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
 50 55 60
 Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
 65 70 75 80
 Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
 85 90 95
 Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala
 100 105 110
 Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn
 115 120 125
 Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
 130 135 140
 Pro His Val Trp Ala Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val
 145 150 155 160
 Phe His Ala Gly His Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro
 165 170 175
 Pro Pro Pro Gly Ser Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly
 180 185 190
 Pro Val Val Gly Val Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys
 195 200 205
 Ile Ile Thr Gly Val Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr
 210 215 220
 Ser Ser Leu Asp Gly Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro
 225 230 235 240
 Glu Val Leu Glu Arg Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser
 245 250 255
 Gly Gly Phe Gly Glu Val Leu Asp Val Pro Arg Val Ser Ala Leu Val
 260 265 270
 Asp Gly Val Ser Leu Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala
 275 280 285
 Tyr Ser Ile Pro Gly Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu
 290 295 300

Gly Ala Ile Pro Pro Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr
305 310 315 320

Cys Ala Ala Gly Val Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser
325 330 335

Ala Gly Tyr Thr Gly Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp
340 345 350

Leu Asp Ser Leu Gly
355

<210> 735

<211> 497

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (7)..(474)

<223> FRXA02802

<400> 735

tccgcgatg gcc atg gaa gcc ctg aaa atc atc acc ggc gtg ggc aca ccc 51
Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro
1 5 10 15

ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc acc tgg gaa 99
Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu
20 25 30

tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg gtg ctt ggg 147
Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly
35 40 45

tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag gtg ctc gat 195
Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp
50 55 60

gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tcg ctc atc gac gtc 243
Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val
65 70 75

cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc gcg cac aac 291
Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn
80 85 90 95

acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc tcc gtt tcc 339
Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser
100 105 110

gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc cgc tcc gca 387
Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala
115 120 125

caa gcc atc gca att tta gaa tcc gca ggc tac acc gga atg agc agc 435
Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser
130 135 140

ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg taaaaccaag 484
 Leu Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
 145 150 155

gcgttggtgcc acc 497

<210> 736
 <211> 156
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 736
 Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro Leu
 1 5 10 15
 Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu Tyr
 20 25 30
 Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly Ser
 35 40 45
 Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp Val
 50 55 60
 Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val Arg
 65 70 75 80
 Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn Thr
 85 90 95
 Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser Ala
 100 105 110
 Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala Gln
 115 120 125
 Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser Leu
 130 135 140
 Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
 145 150 155

<210> 737
 <211> 535
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(535)
 <223> FRXA00438

<400> 737
 ccttcgccgc ctgctccgac ctgcgccgac ccgtcaaagc ccaggtcccg atctggaaag 60
 agcaaacgcg cctcgacggc tccaccgatt gggtcggcct gtg aaa aac ctc gac 115
 Val Lys Asn Leu Asp
 1 5

atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163
 Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln
 10 15 20

 aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211
 Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly
 25 30 35

 ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259
 Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly
 40 45 50

 cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307
 His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His
 55 60 65

 cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355
 Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu
 70 75 80 85

 tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403
 Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr
 90 95 100

 gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451
 Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala
 105 110 115

 gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
 120 125 130

 ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc 535
 Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro
 135 140 145

<210> 738

<211> 145

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 738

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
 1 5 10 15

 Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
 20 25 30

 Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
 35 40 45

 Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
 50 55 60

 Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
 65 70 75 80

 Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
 85 90 95

Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala
 100 105 110

Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn
 115 120 125

Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
 130 135 140

Pro
 145

<210> 739

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXN00437

<400> 739

ttcatcatgg cgctgcccgg ctccacgggt gcggcgcgcg atgccaccgc tgtcctcgac 60

ccactcattg atcacatcac tggaactctg caaggccacc atg aac act gac ccc 115
 Met Asn Thr Asp Pro
 1 5

gct tac gtc gcc gaa caa acc ggc aaa ctc atc gac gct ttc ctc acc 163
 Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile Asp Ala Phe Leu Thr
 10 15 20

acc gac ccc ctc gaa ccg ctg ctc gac gcc gcc aaa aac ggc gtc tgc 211
 Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala Lys Asn Gly Val Cys
 25 30 35

aca gag gcg atg ggc gcg ctg gtc acc ttc gaa ggc atc gtc cgc gac 259
 Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu Gly Ile Val Arg Asp
 40 45 50

cac gac ggc ggc gcc cgc gtg acc tcc ctg acc tac acc gcg cat ccc 307
 His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr Tyr Thr Ala His Pro
 55 60 65

acc gcg ccg cag gtc ctt tct gct gtc gcg gac tcc atc gtt gaa aaa 355
 Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp Ser Ile Val Glu Lys
 70 75 80 85

cac ccg cgc acc cgc ctc tgg acc gcg cac cgc acc ggc gcc ttg aaa 403
 His Pro Arg Thr Arg Leu Trp Thr Ala His Arg Thr Gly Ala Leu Lys
 90 95 100

atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc tcc gcc cac cgc gcc 451
 Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala Ser Ala His Arg Ala
 105 110 115

gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac gcc gtc aaa gcc cag 499
 Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp Ala Val Lys Ala Gln
 120 125 130

gtc ccg atc tgg aaa gag caa acg cgc ctc gac ggc tcc acc gat tgg 547
 Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp Gly Ser Thr Asp Trp
 135 140 145

gtc ggc ctg tgaaaaacct cgacatcgcc cgc 579
 Val Gly Leu
 150

<210> 740

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 740

Met Asn Thr Asp Pro Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile
 1 5 10 15

Asp Ala Phe Leu Thr Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala
 20 25 30

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 35 40 45

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 50 55 60

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 65 70 75 80

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 85 90 95

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 100 105 110

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 115 120 125

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 130 135 140

Gly Ser Thr Asp Trp Val Gly Leu
 145 150

<210> 741

<211> 383

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(360)

<223> FRXA00437

<400> 741

aaa aac ggc gtc tgc aca gag gcg atg ggc gcg ctg gtc acc ttc gaa 48
 Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 1 5 10 15

```

ggc atc gtc cgc gac cac gac ggc ggc gcc cgc gtg acc tcc ctg acc 96
Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
      20      25      30

tac acc gcg cat ccc acc gcg ccg cag gtc ctt tct gct gtc gcg gac 144
Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
      35      40      45

tcc atc gtt gaa aaa cac ccg cgc acc cgc ctc tgg acc gcg cac cgc 192
Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
      50      55      60

acc ggc gcc ttg aaa atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc 240
Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
      65      70      75      80

tcc gcc cac cgc gcc gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac 288
Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
      85      90      95

gcc gtc aaa gcc cag gtc ccg atc tgg aaa gag caa acg cgc ctc gac 336
Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
      100      105      110

ggc tcc acc gat tgg gtc ggc ctg tgaaaaaacct cgacatcgcc cgc 383
Gly Ser Thr Asp Trp Val Gly Leu
      115      120

```

<210> 742

<211> 120

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 742

```

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
  1              5              10              15

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
      20      25      30

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
      35      40      45

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
      50      55      60

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
      65      70      75      80

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
      85      90      95

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
      100      105      110

Gly Ser Thr Asp Trp Val Gly Leu
      115      120

```



```
<210> 743
<211> 591
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(568)  
<223> RXN00439
```

<400> 743																
ctgccaccgc agactgtctg atcaggatcc cggcgcggac tacggtggag gaaaacgaca 60																
tcgttaagat ttacccattc aactaacagg agttaattta atg agc gag ctc acc 115																
Met Ser Glu Leu Thr 5																
cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163																
His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys 20																
aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211																
Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg 35																
ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggc gac 259																
Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp 50																
gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307																
Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr 65																
ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355																
Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr 85																
gtg gat ttt ttt gag ctt act gat ggt gtt cgg att gag gct tcg gtg 403																
Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg Ile Glu Ala Ser Val 100																
aaa acg cgt ggg gtt act ggt gtg gaa atg gag gcg ttg acg gcc gtg 451																
Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu Ala Leu Thr Ala Val 115																
agc act gcg gcg ctg acg gta tac gac atg atc aag gct gtg gat aag 499																
Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile Lys Ala Val Asp Lys 130																
atg gcc gtg att gat ggc att cgt gtg ctg tcg aaa act ggc ggt aaa 547																
Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser Lys Thr Gly Gly Lys 145																
tct ggg gat tgg tct gtt cag tgacagctct gggtatcggt gcg 591																
Ser Gly Asp Trp Ser Val Gln 155																

```
<210> 744
<211> 156
<212> PRT
```

<213> *Corynebacterium glutamicum*

<400> 744

```

Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val
  1              5              10              15

Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly
          20              25              30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly
          35              40              45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met
          50              55              60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro
          65              70              75              80

Leu Gly Lys Ile Thr Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg
          85              90              95

Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu
          100              105              110

Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile
          115              120              125

Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser
          130              135              140

Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val Gln
          145              150              155

```

<210> 745

<211> 218

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(195)

<223> FRXA00439

<400> 745

```

act gat ggt gtt cgg att gag gct tcg gtg aaa acg cgt ggg gtt act   48
Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
  1              5              10              15

ggt gtg gaa atg gag gcg ttg acg gcc gtg agc act gcg gcg ctg acg   96
Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
          20              25              30

gta tac gac atg atc aag gct gtg gat aag atg gcc gtg att gat ggc   144
Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
          35              40              45

att cgt gtg ctg tcg aaa act ggc ggt aaa tct ggg gat tgg tct gtt   192
Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
          50              55              60

```

cag tgacagctct gggtatcggt gcg
Gln
65

218

<210> 746
<211> 65
<212> PRT
<213> Corynebacterium glutamicum

<400> 746
Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
1 5 10 15
Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
20 25 30
Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
35 40 45
Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
50 55 60

Gln
65

<210> 747
<211> 358
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(358)
<223> FRXA00442

<400> 747
ctgccaccgc agactgtctg atcaggatcc cggcgcgaggac tacggtggag gaaaacgaca 60
tcgttaagat ttacccattc aactaacagg agttaattta atg agc gag ctc acc 115
Met Ser Glu Leu Thr
1 5
cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163
His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys
10 15 20
aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211
Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg
25 30 35
ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggg gac 259
Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp
40 45 50
gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307
Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr
55 60 65
ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355

Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr
 70 75 80 85

gtg
 Val

358

<210> 748

<211> 86

<212> PRT

<213> Corynebacterium glutamicum

<400> 748

Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val
 1 5 10 15

Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly
 20 25 30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly
 35 40 45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met
 50 55 60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro
 65 70 75 80

Leu Gly Lys Ile Thr Val
 85

<210> 749

<211> 582

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(559)

<223> RXA00440

<400> 749

cgttatcacga catgatcaag gctgtggata agatggccgt gattgatggc attcgtgtgc 60

tgtcgaaaac tggcggtaaa tctggggatt ggtctgttca gtg aca gct ctg gtt 115
 Val Thr Ala Leu Val
 1 5

atc gtt gcg tcc act cgc gcc gct gcc ggg gtg tat gag gat cgc tct 163
 Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val Tyr Glu Asp Arg Ser
 10 15 20

ggc cca att ttg gtg tcg tgg ctg cgt gca aaa ggt ttt gac aca ccc 211
 Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys Gly Phe Asp Thr Pro
 25 30 35

gcc ccc gtg atc gtg gcg gac gcc aac ctg ccc gca ttc ctg gac gag 259
 Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro Ala Phe Leu Asp Glu
 40 45 50

ctg gaa ttt ccg cag gta gta ctt att tca ggc ggc acc gga ctc acg 307
 Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly Gly Thr Gly Leu Thr
 55 60 65
 cct gat gac atc acc gtg gac act tta atc ccg cgc ctc gac aaa gaa 355
 Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro Arg Leu Asp Lys Glu
 70 75 80 85
 atc ccc ggc atc gcc cac gct ttt tgg aat tac agc atg gac gcc gtc 403
 Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr Ser Met Asp Ala Val
 90 95 100
 ccg acc gca gta ttg tcg cgc acc gtc gcg ggc acc atc ggc ggc agt 451
 Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly Thr Ile Gly Gly Ser
 105 110 115
 ttc atc atg gcg ctg ccc ggc tcc acg ggt gcg gcg cgc gat gcc acc 499
 Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala Ala Arg Asp Ala Thr
 120 125 130
 gct gtc ctc gac cca ctc att gat cac atc act gga act ctg caa ggc 547
 Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr Gly Thr Leu Gln Gly
 135 140 145
 cac cat gaa cac tgaccccgct tacgtcgccg aac 582
 His His Glu His
 150

<210> 750

<211> 153

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 750

Val Thr Ala Leu Val Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val
 1 5 10 15
 Tyr Glu Asp Arg Ser Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys
 20 25 30
 Gly Phe Asp Thr Pro Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro
 35 40 45
 Ala Phe Leu Asp Glu Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly
 50 55 60
 Gly Thr Gly Leu Thr Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro
 65 70 75 80
 Arg Leu Asp Lys Glu Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr
 85 90 95
 Ser Met Asp Ala Val Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly
 100 105 110
 Thr Ile Gly Gly Ser Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala
 115 120 125
 Ala Arg Asp Ala Thr Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr

130 135 140

Gly Thr Leu Gln Gly His His Glu His
145 150

<210> 751
<211> 1287
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(1264)
<223> RXN00441

<400> 751
agccttgagg gcggtgatta tgcttttggc tgtctatgtc ctcatcattg gagccatcgg 60

agcggttacga ttgttttcca aggtgagaaa ggtttaattg atg tct cgt tcg ccg 115
Met Ser Arg Ser Pro
1 5

gag caa cat ttg gca gaa att tca gcg ctg ctt ccc cca caa aag tcc 163
Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu Pro Pro Gln Lys Ser
10 15 20

acg ttc gtg aat ctg cgc gaa gcg ttg gga cgc cgc acg ttt tca gcg 211
Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg Arg Thr Phe Ser Ala
25 30 35

gtc act gcg cag tgg gat tcg cca cgt ttt gat aat tcc caa atg gat 259
Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp Asn Ser Gln Met Asp
40 45 50

ggc ttc gcg ctt ggc ccc tca cat ctt aac ggt ggc acc ttc gca gtc 307
Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly Gly Thr Phe Ala Val
55 60 65

ggt cca acc att ccc gct ggt cat gat cct gat cag tgg tac cca cga 355
Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp Gln Trp Tyr Pro Arg
70 75 80 85

ggc atc gaa aaa gac atc gcg ccg att atg acg ggt gcg cgc ctt cct 403
Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr Gly Ala Arg Leu Pro
90 95 100

aaa aac acc gcc gcg atc att cct gtg gag aaa acc aca ccg gga aat 451
Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys Thr Thr Pro Gly Asn
105 110 115

ttc gac gcc cca cag gta gaa atc ccc gcc acc ccg caa ggt cag ttc 499
Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr Pro Gln Gly Gln Phe
120 125 130

ata cgg ttg cag ggt tcg gat att act gcc ggc gac gag atc att cca 547
Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly Asp Glu Ile Ile Pro
135 140 145

gca ggt acg gag ctt aac tcg gtg cac atc ggg gtg ttg gct agt cag 595
Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly Val Leu Ala Ser Gln

150	155	160	165	
tcg atc aag agc att gaa gtc gca gca aag cca cgt gtc ctc atc atc				643
Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro Arg Val Leu Ile Ile	170	175	180	
acc ggc ggg tct gaa att tca gaa cag cac gga ccc gcc acg atc cct				691
Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly Pro Ala Thr Ile Pro	185	190	195	
gat gcc aac ggc cct ctg ctt cgt tcc ctg tgc gcc cgc aac aat atc				739
Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys Ala Arg Asn Asn Ile	200	205	210	
gag gtc atc gcg gga ctg cac acc aac gac gat cct gaa cga ctc cgc				787
Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp Pro Glu Arg Leu Arg	215	220	225	
ttt gaa ctg gaa aac gcc att gac cag tat caa ccg gat gtc atc atc				835
Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln Pro Asp Val Ile Ile	230	235	240	245
acc tct ggc ggt atc agc cac ggt aaa ttt gag gtg ttt agg cag atc				883
Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu Val Phe Arg Gln Ile	250	255	260	
ctc gaa ggc acc ccg aac tcc tgg ttt gga cat gtc gat cag cag cct				931
Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His Val Asp Gln Gln Pro	265	270	275	
ggc ggt cct caa ggc atc tcc act ttt gct gaa act cct gtc att tca				979
Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu Thr Pro Val Ile Ser	280	285	290	
ctt ccc gga aat ccg att tcc acc ttg gtg agt ttc aca ctt ttg gtc				1027
Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser Phe Thr Leu Leu Val	295	300	305	
gcg cca gcg ctc aac cgc cag ccg ctc cgc cac ctc gat gcc cgc atc				1075
Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His Leu Asp Ala Arg Ile	310	315	320	325
acc gct ccg gtc cag ggc ttg caa gac aat cgc gag caa ttc ctt cgc				1123
Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg Glu Gln Phe Leu Arg	330	335	340	
ggc acc atc agt tac cgc aac ggg cca cgt cct cgc cac gcc tct cct				1171
Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro Arg His Ala Ser Pro	345	350	355	
ggg cac cag ttc cca cct gct ggt tca agc tgc cac cgc aga ctg tct				1219
Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys His Arg Arg Leu Ser	360	365	370	
gat cag gat ccc ggc gcg gac tac ggt gga gga aaa cga cat cgt				1264

Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly Lys Arg His Arg
 375 380 385

taagatttac ccattcaact aac
 1287

<210> 752

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 752

Met Ser Arg Ser Pro Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu
 1 5 10 15

Pro Pro Gln Lys Ser Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg
 20 25 30

Arg Thr Phe Ser Ala Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp
 35 40 45

Asn Ser Gln Met Asp Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly
 50 55 60

Gly Thr Phe Ala Val Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp
 65 70 75 80

Gln Trp Tyr Pro Arg Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr
 85 90 95

Gly Ala Arg Leu Pro Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys
 100 105 110

Thr Thr Pro Gly Asn Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr
 115 120 125

Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly
 130 135 140

Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly
 145 150 155 160

Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro
 165 170 175

Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly
 180 185 190

Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys
 195 200 205

Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp
 210 215 220

Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln
 225 230 235 240

Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu
 245 250 255

Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His
 260 265 270

Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu
 275 280 285

Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser
 290 295 300

Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His
 305 310 315 320

Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg
 325 330 335

Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro
 340 345 350

Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys
 355 360 365

His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly
 370 375 380

Lys Arg His Arg
 385

<210> 753

<211> 815

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(792)

<223> FRXA00441

<400> 753

atc ccc gcc acc ccg caa ggt cag ttc ata cgg ttg cag ggt tcg gat	48
Ile Pro Ala Thr Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp	
1 5 10 15	
att act gcc ggc gac gag atc att cca gca ggt acg gag ctt aac tcg	96
Ile Thr Ala Gly Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser	
20 25 30	
gtg cac atc ggg gtg ttg gct agt cag tcg atc aag agc att gaa gtc	144
Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val	
35 40 45	
gca gca aag cca cgt gtc ctc atc atc acc ggc ggg tct gaa att tca	192
Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser	
50 55 60	
gaa cag cac gga ccc gcc acg atc cct gat gcc aac ggc cct ctg ctt	240
Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu	
65 70 75 80	
cgt tcc ctg tgc gcc cgc aac aat atc gag gtc atc gcg gga ctg cac	288
Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His	

85										90					95					
acc aac gac gat cct gaa cga ctc cgc ttt gaa ctg gaa aac gcc att	336																			
Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile																				
100 105 110																				
gac cag tat caa ccg gat gtc atc atc acc tct ggc ggt atc agc cac	384																			
Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His																				
115 120 125																				
ggt aaa ttt gag gtg ttt agg cag atc ctc gaa ggc acc ccg aac tcc	432																			
Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser																				
130 135 140																				
tgg ttt gga cat gtc gat cag cag cct ggc ggt cct caa ggc atc tcc	480																			
Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser																				
145 150 155 160																				
act ttt gct gaa act cct gtc att tca ctt ccc gga aat ccg att tcc	528																			
Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser																				
165 170 175																				
acc ttg gtg agt ttc aca ctt ttg gtc gcg cca gcg ctc aac cgc cag	576																			
Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln																				
180 185 190																				
ccg ctc cgc cac ctc gat gcc cgc atc acc gct ccg gtc cag ggc ttg	624																			
Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu																				
195 200 205																				
caa gac aat cgc gag caa ttc ctt cgc ggc acc atc agt tac cgc aac	672																			
Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn																				
210 215 220																				
ggg cca cgt cct cgc cac gcc tct cct ggg cac cag ttc cca cct gct	720																			
Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala																				
225 230 235 240																				
ggt tca agc tgc cac cgc aga ctg tct gat cag gat ccc ggc gcg gac	768																			
Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp																				
245 250 255																				
tac ggt gga gga aaa cga cat cgt taagatttac ccattcaact aac	815																			
Tyr Gly Gly Gly Lys Arg His Arg																				
260																				

<210> 754

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 754

Ile	Pro	Ala	Thr	Pro	Gln	Gly	Gln	Phe	Ile	Arg	Leu	Gln	Gly	Ser	Asp
1				5					10					15	

Ile	Thr	Ala	Gly	Asp	Glu	Ile	Ile	Pro	Ala	Gly	Thr	Glu	Leu	Asn	Ser
		20						25					30		

Val	His	Ile	Gly	Val	Leu	Ala	Ser	Gln	Ser	Ile	Lys	Ser	Ile	Glu	Val
		35					40					45			

Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser
50 55 60

Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu
65 70 75 80

Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His
85 90 95

Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile
100 105 110

Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His
115 120 125

Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser
130 135 140

Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser
145 150 155 160

Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser
165 170 175

Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln
180 185 190

Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu
195 200 205

Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn
210 215 220

Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala
225 230 235 240

Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp
245 250 255

Tyr Gly Gly Gly Lys Arg His Arg
260

<210> 755

<211> 2358

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2335)

<223> RXN02085

<400> 755

caccgcgtga tttcgcgaac cttgaaacat cgtcagaaga ttgccgtgcg tcctagccgg 60

gatccgcacg ttcgggtcaa gcagaaagtc tttaactcac atg act tcc aac ttt 115
Met Thr Ser Asn Phe
1 5

tct	tcc	act	gtc	gct	ggt	ctt	cct	cgc	atc	gga	gcg	aag	cgt	gaa	ctg	163
Ser	Ser	Thr	Val	Ala	Gly	Leu	Pro	Arg	Ile	Gly	Ala	Lys	Arg	Glu	Leu	
				10					15					20		
aag	ttc	gcg	ctc	gaa	ggc	tac	tgg	aat	gga	tca	att	gaa	ggt	cgc	gaa	211
Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu	
			25					30					35			
ctt	gcg	cag	acc	gcc	cgc	caa	ttg	gtc	aac	act	gca	tcg	gat	tct	ttg	259
Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr	Ala	Ser	Asp	Ser	Leu	
			40				45					50				
tct	gga	ttg	gat	tcc	gtt	ccg	ttt	gca	gga	cgt	tcc	tac	tac	gac	gca	307
Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg	Ser	Tyr	Tyr	Asp	Ala	
	55					60					65					
atg	ctc	gat	acc	gcc	gct	att	ttg	ggt	gtg	ctg	ccg	gag	cgt	ttt	gat	355
Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu	Pro	Glu	Arg	Phe	Asp	
	70				75					80					85	
gac	atc	gct	gat	cat	gaa	aac	gat	ggt	ctc	cca	ctg	tgg	att	gac	cgc	403
Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro	Leu	Trp	Ile	Asp	Arg	
				90					95					100		
tac	ttt	ggc	gct	gct	cgc	ggt	act	gag	acc	ctg	cct	gca	cag	gca	atg	451
Tyr	Phe	Gly	Ala	Ala	Arg	Gly	Thr	Glu	Thr	Leu	Pro	Ala	Gln	Ala	Met	
			105					110					115			
acc	aag	tgg	ttt	gat	acc	aac	tac	cac	tac	ctc	gtg	ccg	gag	ttg	tct	499
Thr	Lys	Trp	Phe	Asp	Thr	Asn	Tyr	His	Tyr	Leu	Val	Pro	Glu	Leu	Ser	
		120					125					130				
gcg	gat	aca	cgt	ttc	gtt	ttg	gat	gcg	tcc	gcg	ctg	att	gag	gat	ctc	547
Ala	Asp	Thr	Arg	Phe	Val	Leu	Asp	Ala	Ser	Ala	Leu	Ile	Glu	Asp	Leu	
	135					140					145					
cgt	tgc	cag	cag	gtt	cgt	ggc	gtt	aat	gcc	cgc	cct	gtt	ctg	gtt	ggt	595
Arg	Cys	Gln	Gln	Val	Arg	Gly	Val	Asn	Ala	Arg	Pro	Val	Leu	Val	Gly	
	150				155					160					165	
cca	ctg	act	ttc	ctt	tcc	ctt	gct	cgc	acc	act	gat	ggt	tcc	aat	cct	643
Pro	Leu	Thr	Phe	Leu	Ser	Leu	Ala	Arg	Thr	Thr	Asp	Gly	Ser	Asn	Pro	
				170					175					180		
ttg	gat	cac	ctg	cct	gca	ctg	ttt	gag	gtc	tac	gag	cgc	ctc	atc	aag	691
Leu	Asp	His	Leu	Pro	Ala	Leu	Phe	Glu	Val	Tyr	Glu	Arg	Leu	Ile	Lys	
			185					190					195			
tct	ttc	gat	act	gag	tgg	gtt	cag	atc	gat	gag	cct	gcg	ttg	gtc	acc	739
Ser	Phe	Asp	Thr	Glu	Trp	Val	Gln	Ile	Asp	Glu	Pro	Ala	Leu	Val	Thr	
		200				205						210				
gat	gtt	gct	cct	gag	gtt	ttg	gag	cag	gtc	cgc	gct	ggt	tac	acc	act	787
Asp	Val	Ala	Pro	Glu	Val	Leu	Glu	Gln	Val	Arg	Ala	Gly	Tyr	Thr	Thr	
	215					220					225					
ttg	gct	aag	cgc	gat	ggc	gtg	ttt	gtc	aat	act	tac	ttc	ggc	tct	ggc	835
Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr	Tyr	Phe	Gly	Ser	Gly	
	230				235					240					245	
gat	cag	gcg	ctg	aac	act	ctt	gcg	ggc	atc	ggc	ctt	ggc	gcg	att	ggc	883

```

Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly
      250                      255                      260

ggt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly
      265                      270                      275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
      280                      285                      290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc
1027
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
      295                      300                      305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac
1075
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
      310                      315                      320                      325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
1123
Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
      330                      335                      340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
1171
Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
      345                      350                      355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
1219
Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
      360                      365                      370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
1267
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
      375                      380                      385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
1315
Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
      390                      395                      400                      405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
1363
Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
      410                      415                      420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
1411
Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
      425                      430                      435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
1459
Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
      440                      445                      450

```

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
250 255 260	
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc	
1027	
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
295 300 305	
ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac	
1075	
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	
acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc	
1123	
Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala	
330 335 340	
ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta	
1171	
Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu	
345 350 355	
gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att	
1219	
Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile	
360 365 370	
gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc	
1267	
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu	
375 380 385	
cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag	
1315	

gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc
2083

Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu
650 655 660

gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg
2131

Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val
665 670 675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt
2179

Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly
680 685 690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc
2227

Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val
695 700 705

aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct
2275

Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc
2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
730 735 740

gga gca act atc taaattgggt taccgctagg aac
2358

Gly Ala Thr Ile
745

<210> 756

<211> 745

<212> PRT

<213> Corynebacterium glutamicum

<400> 756

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu

100	105	110
Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu 115	120	125
Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala 130	135	140
Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg 145	150	155
Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr 165	170	175
Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr 180	185	190
Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu 195	200	205
Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg 210	215	220
Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr 225	230	235
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly 245	250	255
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu 260	265	270
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly 275	280	285
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys 290	295	300
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu 305	310	315
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val 325	330	335
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu 340	345	350
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala 355	360	365
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro 370	375	380
Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg 385	390	395
Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr 405	410	415
Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala 420	425	430

Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
 580 585 590
 Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
 595 600 605
 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
 610 615 620
 Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
 625 630 635 640
 Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
 645 650 655
 Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
 660 665 670
 Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
 675 680 685
 Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
 690 695 700
 Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
 705 710 715 720
 Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln
 725 730 735
 Ala Arg Glu Lys Ile Gly Ala Thr Ile
 740 745

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
250 255 260	
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc	
1027	
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
295 300 305	
ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac	
1075	
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	
acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc	
1123	
Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala	
330 335 340	
ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta	
1171	
Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu	
345 350 355	
gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att	
1219	
Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile	
360 365 370	
gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc	
1267	
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu	
375 380 385	
cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag	
1315	

Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405
 aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
 1363
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420
 cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
 1411
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435
 tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450
 ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
 1507
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
 455 460 465
 ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc
 1555
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
 470 475 480 485
 gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc
 1603
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
 490 495 500
 cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
 1651
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
 505 510 515
 cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
 520 525 530
 cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc
 1747
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
 535 540 545
 ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca
 1795
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
 550 555 560 565
 ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag
 1843
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
 570 575 580
 atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg
 1891
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr

585

590

595

aga cgt cga taagcctgcc tacctgcagt ggt

1923

Arg Arg Arg

600

<210> 758

<211> 600

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 758

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
1 5 10 15Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
20 25 30Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
100 105 110Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
115 120 125Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
130 135 140Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
145 150 155 160Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
165 170 175Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
180 185 190Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
195 200 205Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
210 215 220Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
225 230 235 240Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
245 250 255

Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
580 585 590

Leu Leu Pro Ala Thr Arg Arg Arg
595 600

<210> 759

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> FRXA02086

<400> 759

gatgatcagc cgctggctac cactgctgac caggttgac tggcactgcg cgatgaaatt 60

aacgatctca tcgaggctgg cgcgaagatc atccaggtgg atg agc ctg cga ttc 115
Met Ser Leu Arg Phe
1 5

gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
10 15 20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
25 30 35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
40 45 50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
55 60 65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
70 75 80 85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
90 95 100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
105 110 115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
120 125 130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
135 140 145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600

Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
 150 155 160

aac

603

<210> 760
 <211> 160
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 760
 Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
 1 5 10 15
 Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
 20 25 30
 Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
 35 40 45
 Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
 50 55 60
 Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
 115 120 125
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
 130 135 140
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
 145 150 155 160

<210> 761
 <211> 1326
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1303)
 <223> RXN02648

<400> 761
 atgaataaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcggttag agtcgaatga 60
 gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115
 Met Ser Gln Asn Arg

																1	5
atc	agg	acc	act	cac	gtt	ggg	tcc	ttg	ccc	cgt	acc	cca	gag	cta	ctt	163	
Ile	Arg	Thr	Thr	His	Val	Gly	Ser	Leu	Pro	Arg	Thr	Pro	Glu	Leu	Leu		
				10					15					20			
gat	gca	aac	atc	aag	cgt	tct	aac	ggg	gag	att	ggg	gag	gag	gaa	ttc	211	
Asp	Ala	Asn	Ile	Lys	Arg	Ser	Asn	Gly	Glu	Ile	Gly	Glu	Glu	Glu	Phe		
				25					30					35			
ttc	cag	att	ctg	cag	tct	tct	gta	gat	gac	gtg	atc	aag	cgc	cag	gtt	259	
Phe	Gln	Ile	Leu	Gln	Ser	Ser	Val	Asp	Asp	Val	Ile	Lys	Arg	Gln	Val		
				40					45					50			
gac	ctg	ggg	atc	gac	atc	ctt	aac	gag	ggc	gaa	tac	ggc	cac	gtc	acc	307	
Asp	Leu	Gly	Ile	Asp	Ile	Leu	Asn	Glu	Gly	Glu	Tyr	Gly	His	Val	Thr		
				55					60					65			
tcc	ggg	gca	gtt	gac	ttc	ggg	gca	tgg	tgg	aac	tac	tcc	ttc	acc	cgc	355	
Ser	Gly	Ala	Val	Asp	Phe	Gly	Ala	Trp	Trp	Asn	Tyr	Ser	Phe	Thr	Arg		
				70					75					80			
ctg	ggc	gga	ctg	acc	atg	acc	gat	acc	gac	cgt	tgg	gca	agc	cag	gaa	403	
Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg	Trp	Ala	Ser	Gln	Glu		
				90					95					100			
gca	gtg	cgt	tcc	acc	cct	ggc	aac	atc	gag	ctg	acc	agc	ttc	tct	gat	451	
Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu	Thr	Ser	Phe	Ser	Asp		
				105					110					115			
cgt	cgc	gac	cgc	gca	ttg	ttc	agc	gaa	gca	tac	gag	gat	cca	gta	tct	499	
Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr	Glu	Asp	Pro	Val	Ser		
				120					125					130			
ggc	atc	ttc	acc	ggg	cgc	gct	tct	gtg	ggc	aac	cca	gag	ttc	acc	gga	547	
Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn	Pro	Glu	Phe	Thr	Gly		
				135					140					145			
cct	att	acc	tac	att	ggc	cag	gaa	gaa	act	cag	acg	gat	gtt	gat	ctg	595	
Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Val	Asp	Leu		
				150					155					160			
ctg	aag	aag	ggc	atg	aac	gca	gcg	gga	gct	acc	gac	ggc	ttc	gtt	gca	643	
Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala		
				170					175					180			
gca	cta	tcc	cca	gga	tct	gca	gct	cga	ttg	acc	aac	aag	ttc	tac	gac	691	
Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp		
				185					190					195			
act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gcg	ctt	tcc	cag	gaa	739	
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu		
				200					205					210			
tac	aag	atc	atc	acc	gat	gca	ggg	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787	
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro		
				215					220					225			
gac	ttg	gca	gaa	gca	tgg	gat	cag	atc	aac	cca	gag	cca	agc	gtg	aag	835	
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys		
				230					235					240			

gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883
 Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala
 250 255 260

gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc 931
 Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly
 265 270 275

tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979
 Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile
 280 285 290

ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca
 1027
 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala
 295 300 305

tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt
 1075
 Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
 310 315 320 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac
 1123
 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
 330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc
 1171
 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
 345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg
 1219
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
 360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta
 1267
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
 375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac
 1313
 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 390 395 400

aacgagggtt gct
 1326

<210> 762
 <211> 401
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 762
 Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly S r Leu Pro Arg
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg

340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400
 Phe

<210> 763
 <211> 548
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(525)
 <223> FRXA02648

<400> 763
 gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca 48
 Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1 5 10 15
 agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30
 aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
 Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45
 tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60
 gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80
 gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95
 aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110
 tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125
 cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

taagctagac aacgagggtt gct 548

<210> 764

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 764

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1 5 10 15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

<210> 765

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658

<400> 765

```

atgaataaaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcgggttag agtcgaatga 60
gagtttgata ctttcttttcg acttttagat tggattttca atg agc cag aac cgc 115
                                         Met Ser Gln Asn Arg
                                         1 5
atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
                        10 15 20
gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
                        25 30 35
ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
                        40 45 50
gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
                        55 60 65
tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
                        70 75 80 85
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
                        90 95 100
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
                        105 110 115
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
                        120 125 130
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
                        135 140 145
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
                        150 155 160 165
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
                        170 175 180
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
                        185 190 195
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
                        200 205 210
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784

```

Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 766

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 766

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220

Gln Leu Asp Ala
 225

<210> 767

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

<223> RXA01516

<400> 767

```

tctgcacata tgggagcatg ggggtgtgctg gtgcacgatg tcccagtatc aaggagcgt 60

gttgatgttg ccgcattgtg gcgaagtgga ggaactcacc atg gct gat cgt att 115
                                         Met Ala Asp Arg Ile
                                         1           5

gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt 163
Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe
                        10                15                20

gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg 211
Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met
                        25                30                35

gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259
Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp
                        40                45                50

tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc 307
Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser
                        55                60                65

agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg 355
Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met
                        70                75                80                85

gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc 403
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro
                        90                95                100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga 451
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg
                        105                110                115

cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc 500
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala
                        120                125                130

agttttgtcc atc 513

```

<210> 768

<211> 130

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 768

```

Met Ala Asp Arg Ile Glu Leu Lys Gly Leu Glu Cys Phe Gly His His
  1           5           10           15

Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp
  20                25                30

Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu
  35                40                45

```


Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile
 50 55 60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser
 65 70 75 80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val
 85 90 95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser
 115 120 125

Asn Ala
 130

<210> 769
 <211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(952)
 <223> RXA01515

<400> 769
 taagcctgggt gctgtgacca cgacgtctgc ggtgcgcggc ggttttaaga acaacgctgc 60

ctccccgcgt gaggtgttct ccctgattcg ggggcactaa atg aac gta tcc tct 115
 Met Asn Val Ser Ser
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr
 10 15 20

gag gat tcc ttt tgc gac ggt ggc aag tac att gac gtt gat cag gcg 211
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu
 105 110 115
 gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
 120 125 130
 tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547
 Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
 135 140 145
 gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
 150 155 160 165
 gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
 170 175 180
 gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
 185 190 195
 cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
 200 205 210
 ctg gtg gga gca tcc cgg aag cga ttc ctg gct gcc gtg cgc aaa gac 787
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
 215 220 225
 cgt gcc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
 230 235 240 245
 gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
 250 255 260
 gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
 265 270 275
 agt gga gga act cac cat gcc tgcgtatt gaacttaaag gcc 975
 Ser Gly Gly Thr His His Gly
 280

<210> 770

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 770

Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly
 1 5 10 15

Ile Val Asn Val Thr Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile
 20 25 30

Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80
 Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala
 85 90 95
 Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp
 100 105 110
 Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu
 115 120 125
 Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly
 130 135 140
 Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val
 145 150 155 160
 His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val
 165 170 175
 Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser
 180 185 190
 Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser
 195 200 205
 Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala
 210 215 220
 Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp
 225 230 235 240
 Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp
 245 250 255
 Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val
 260 265 270
 Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly
 275 280

<210> 771

<211> 859

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA02024

<400> 771

cactgatgac ctggatcagg ccgtcaaatt catcgctgat gcacacgctg gattggacgt 60

agcgcgtctc cacaattaag cagtggctac attaggtggt	atg agt tct ttg ccg	115
	Met Ser Ser Leu Pro	
	1 5	
gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag	163	
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys		
10 15 20		
ggg gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211	
Gly Ala Thr Phe Glu Asp Thr Ala Leu Asn Arg Ala Ala Glu Val		
25 30 35		
att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259	
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly		
40 45 50		
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307	
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro		
55 60 65		
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355	
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val		
70 75 80 85		
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403	
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala		
90 95 100		
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451	
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln		
105 110 115		
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg	499	
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly		
120 125 130		
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547	
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val		
135 140 145		
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595	
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg		
150 155 160 165		
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643	
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe		
170 175 180		
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691	
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu		
185 190 195		
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat	739	
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp		
200 205 210		
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc	787	
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly		
215 220 225		

acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt 835
 Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe
 230 235 240 245

cgc gtg cat gaa gtt gcg gaa acc 859
 Arg Val His Glu Val Ala Glu Thr
 250

<210> 772

<211> 253

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 772

Met Ser Ser Leu Pro Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp
 1 5 10 15

Ser Phe Tyr Asp Lys Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn
 20 25 30

Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly
 35 40 45

Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile
 50 55 60

Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp
 65 70 75 80

Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala
 85 90 95

Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp
 100 105 110

His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys
 115 120 125

Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His
 130 135 140

Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala
 145 150 155 160

Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp
 165 170 175

Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu
 180 185 190

Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala
 195 200 205

Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp
 210 215 220

Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg
 225 230 235 240

Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr

245

250

```
<210> 773
<211> 684
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(661)  
<223> RXA01719
```

<400>	773
c c a t a t g g t c g g t g c a c t g g c t g g a a g t g g c g g t a t t g c a c t g g t g a c t t c g t c g a t t g c	60
c g a g g a c g g t c t g g t t g a t g t t g t g c t g g g g a g a a t g t a a a t g a a t a t c a t c a t t	115
Met Asn Ile Ile Ile 1 5	
c t t g c t g g t g g c g a g g g t a a a c g c a t g g g t g g g g t g g a t a a g g c t g c t	163
Leu Ala Gly Gly Glu Gly Lys Arg Met Gly Gly Val Asp Lys Ala Ala 10 15 20	
g t g g c g g t g g a t g g t c g c a c g c t g c t g g a t a t c c t g c t t t c a c a g c t g	211
Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile Leu Leu Ser Gln Leu 25 30 35	
g a t c c a g a a g a t g a c g t c g t g g t g g t t t c c c c c g c g a t c a t c g a c g g a	259
Asp Pro Glu Asp Asp Val Val Val Val Ser Pro Ala Ile Ile Asp Gly 40 45 50	
a t c a c g a c t g t c t g c g a g g a a c c t c c g c t t g g c g g g c c g g t c g c g g g a	307
Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly Gly Pro Val Ala Gly 55 60 65	
a t c g a g g c a g g g c t g a a t t c t t t t g a g c a c g c c c a t g a a t t c a c t g c g	355
Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala His Glu Phe Thr Ala 70 75 80 85	
a t t c t t g c c g t g g a c g c g c c t t a t t c t g c a g c g a t g c t g c c c c t a c t t	403
Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala Met Leu Pro Leu Leu 90 95 100	
c a g g c a c a g a t t g g c a a a g c c g a t g t g g c c g t a a c c c t t g c t g c c g a t	451
Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val Thr Leu Ala Ala Asp 105 110 115	
g g c t g g g t a c a a c c g t t g t g c g c g c t g t g g a g a a g t g g c a g c c t a g a a	499
Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg Ser Gly Ser Leu Glu 120 125 130	
g c g g t g a t t c a c a g c c t g g g c g a g a c t a g a a a t c g a c c g g c a a a a g c g	547
Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn Arg Pro Ala Lys Ala 135 140 145	
t t a c t g a a g c a a g c g g g a c a c a t t g t g g a a g t g g g t g g c g a t g g c a c t	595
Leu Leu Lys Gln Ala Gly His Ile Val Glu Val Gly Gly Asp Gly Thr 150 155 160 165	
g a a a a a g a c t a c g a t a c g g t g g c t g a a c t g g a g g t a t t g g g c a a c g t a	643

Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu Val Leu Gly Asn Val
 170 175 180

acg ctc cct aaa gcc cac tgatgagaaa cgtgagctct gct
 Thr Leu Pro Lys Ala His
 185

684

<210> 774

<211> 187

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 774

Met Asn Ile Ile Ile Leu Ala Gly Gly Glu Gly Lys Arg Met Gly Gly
 1 5 10 15

Val Asp Lys Ala Ala Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile
 20 25 30

Leu Leu Ser Gln Leu Asp Pro Glu Asp Asp Val Val Val Val Ser Pro
 35 40 45

Ala Ile Ile Asp Gly Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly
 50 55 60

Gly Pro Val Ala Gly Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala
 65 70 75 80

His Glu Phe Thr Ala Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala
 85 90 95

Met Leu Pro Leu Leu Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val
 100 105 110

Thr Leu Ala Ala Asp Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg
 115 120 125

Ser Gly Ser Leu Glu Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn
 130 135 140

Arg Pro Ala Lys Ala Leu Leu Lys Gln Ala Gly His Ile Val Glu Val
 145 150 155 160

Gly Gly Asp Gly Thr Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu
 165 170 175

Val Leu Gly Asn Val Thr Leu Pro Lys Ala His
 180 185

<210> 775

<211> 1332

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1309)

<223> RXA01720

<400> 775

```

acacccggttt gagaatctca acctcttaaa acagcgcgaa ctattgattt ggcaactacc 60

ctatatattt gagtgtttat tgtcgaaaaa ggggtttcaa gtg gca cag caa cgc 115
                               Val Ala Gln Gln Arg
                               1 5

agc gtc gat gac tat ctt tcc att ttg ata gac agc gtc gca ccg ctt 163
Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp Ser Val Ala Pro Leu
                               10 15 20

ccg cca gta aaa acc cct atc ctc ggc gcg cat ccg tta agt cac ctt 211
Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His Pro Leu Ser His Leu
                               25 30 35

gca gag gat gtt gtc gcg aca att cct atc ccg aaa ttt act aat tct 259
Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro Lys Phe Thr Asn Ser
                               40 45 50

gct gtt gat ggt tac gcc att ttg aaa gaa gac atc cat ggc agc ggg 307
Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp Ile His Gly Ser Gly
                               55 60 65

ccg tgg aca ttt ctt gtg ggc ggt gat act ccg gcg ggt tct gcg ccg 355
Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro Ala Gly Ser Ala Pro
70 75 80 85

gcg agc att aat aat gga aaa gcc atc cgt gtg atg aca ggt gga ccc 403
Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val Met Thr Gly Gly Pro
90 95 100

gtc cca tcc acc aac aag gac atg atc gtg gtt cca gtg gag ctc acc 451
Val Pro Ser Thr Asn Lys Asp Met Ile Val Val Pro Val Glu Leu Thr
105 110 115

aat gct ccg gtg gat cac tcg ctt cct aca gaa atc acg atc aat gag 499
Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu Ile Thr Ile Asn Glu
120 125 130

cta cca ggt gag agg aat aat att cgc cat gct ggt gag cat ctt aaa 547
Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala Gly Glu His Leu Lys
135 140 145

gaa ggc gaa att gcg gtt gct gcg ggg acg gca ttt gat gcg ggt act 595
Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala Phe Asp Ala Gly Thr
150 155 160 165

gtg tcg acg gtg att tca gtt ggc cat gac act gta aaa gcc cat cct 643
Val Ser Thr Val Ile Ser Val Gly His Asp Thr Val Lys Ala His Pro
170 175 180

tgc cct cgg gtt gcg gtg atc act acc ggt gat gag cta aac cag gga 691
Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp Glu Leu Asn Gln Gly
185 190 195

aat ccc tgg ggt atc cct aat tcc aat ggg ccg atg ctg gtt gcg gag 739
Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro Met Leu Val Ala Glu
200 205 210

cta aaa cgc gtg ggg att aag gat ccg cag cat ttc cat tcc gat gat 787
Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His Phe His Ser Asp Asp

```


215	220	225	
tct gag act gca ttg agg gag acg ctc gat aag cct gca gag gtt gcg Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys Pro Ala Glu Val Ala 230 235 240 245			835
gat gtg atc atc act gtg ggt ggg atc tcg gcg ggc gcg ttc gat gtg Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala Gly Ala Phe Asp Val 250 255 260			883
gtc aaa gcc gtg gga act aag act ggt ggt ttt gaa ttc ttc ccc att Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe Glu Phe Phe Pro Ile 265 270 275			931
gcg atg aag ccg ggt aaa ccg caa ggt cat ggg cag tgg ggc gac gca Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly Gln Trp Gly Asp Ala 280 285 290			979
aaa gtg gtg tgt ctg ccg gga aac ccg gtg gcg gcg tgg gtt agt ttt 1027 Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala Ala Trp Val Ser Phe 295 300 305			
agg ctc ttt gtt gtt ccg gta att gag aga tta ggg ggt gga aag agg 1075 Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu Gly Gly Gly Lys Arg 310 315 320 325			
ctg gcg tcg ata agc gaa ctc cct gtg gtg gcg ctg cgc tcg aac ccg 1123 Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala Leu Arg Ser Asn Arg 330 335 340			
gcg ctg aag gcg cgg gag ggc ccc gta ttg gcg ata ccg gtg gcg att 1171 Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala Ile Pro Val Ala Ile 345 350 355			
gat tgg gag aaa aga atg gca aat tct cag gca cat cga tcc cat atg 1219 Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala His Arg Ser His Met 360 365 370			
gtc ggt gca ctg gct gga agt ggc ggt att gca ctg gtg act tcg tcg 1267 Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala Leu Val Thr Ser Ser 375 380 385			
att gcc gag gac ggt ctg gtt gat gtt gtg ctg ggg aga atg 1309 Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu Gly Arg Met 390 395 400			
taaataaata tcatcattct tgc 1332			

<210> 776

<211> 403

<212> PRT

<213> Corynebacterium glutamicum

<400> 776

Val Ala Gln Gln Arg Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp
 1 5 10 15
 Ser Val Ala Pro Leu Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His
 20 25 30
 Pro Leu Ser His Leu Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro
 35 40 45
 Lys Phe Thr Asn Ser Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp
 50 55 60
 Ile His Gly Ser Gly Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro
 65 70 75 80
 Ala Gly Ser Ala Pro Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val
 85 90 95
 Met Thr Gly Gly Pro Val Pro Ser Thr Asn Lys Asp Met Ile Val Val
 100 105 110
 Pro Val Glu Leu Thr Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu
 115 120 125
 Ile Thr Ile Asn Glu Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala
 130 135 140
 Gly Glu His Leu Lys Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala
 145 150 155 160
 Phe Asp Ala Gly Thr Val Ser Thr Val Ile Ser Val Gly His Asp Thr
 165 170 175
 Val Lys Ala His Pro Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp
 180 185 190
 Glu Leu Asn Gln Gly Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro
 195 200 205
 Met Leu Val Ala Glu Leu Lys Arg Val Gly Ile Lys Asp Pro Gln His
 210 215 220
 Phe His Ser Asp Asp Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys
 225 230 235 240
 Pro Ala Glu Val Ala Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala
 245 250 255
 Gly Ala Phe Asp Val Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe
 260 265 270
 Glu Phe Phe Pro Ile Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly
 275 280 285
 Gln Trp Gly Asp Ala Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala
 290 295 300
 Ala Trp Val Ser Phe Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu
 305 310 315 320

[illegible]

```
<210> 777
<211> 1237
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (2)..(1207)  
<223> RXS03223
```

<400> 777																
tcca	gag	cca	gtg	cgt	att	gct	att	gca	gag	gca	ctg	ggt	ttg	atg	tgc	49
Pro	Glu	Pro	Val	Arg	Ile	Ala	Ile	Ala	Glu	Ala	Leu	Gly	Leu	Met	Cys	
1				5					10					15		
gcg	gaa	gag	gtt	caa	gct	agt	cgt	gct	ttg	ccg	ggt	ttc	gcg	caa	gca	97
Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala	
			20					25					30			
gcg	att	gat	ggt	tat	gcg	gtt	cga	gca	gtc	gat	gtc	ggc	ggc	gag	aag	145
Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys	
		35					40					45				
tcg	ttt	agc	cag	caa	ctg	ccg	gtt	gct	cct	ccg	gaa	aaa	tcc	ctg	ccc	193
Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro	
	50					55					60					
gtg	gtg	ggt	gaa	gta	gct	gcg	ggt	tct	cag	cag	ccg	ttg	cgc	ctg	cag	241
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln	
65					70					75					80	
cct	aaa	caa	gca	gtc	atg	gtc	cac	acc	ggt	gcg	cca	ctg	ccg	atg	ctt	289
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu	
				85					90					95		
gcg	gat	gcg	gtg	ctg	ccc	atg	gcg	tgg	tca	gat	cgt	ggc	cgc	aaa	cga	337
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg	
			100					105					110			
gta	acc	gcg	cag	cga	cct	gtg	cgc	tct	ggc	gag	ttt	gtg	cgc	aaa	gaa	385
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu	

115	120	125	
ggc gat gac atc caa ccg gga gac atc gca gtc agc gcc ggc gcg gtc Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val 130 135 140			433
tta ggc cct gcc caa att ggt ttg ctc gca gct gtt ggt cgc tcc aaa Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys 145 150 155 160			481
gtg ttg gtg tac cca cgc cca cgc atg tcg gtt atc tcc gta ggc gct Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala 165 170 175			529
gaa ctt gtt gat att gat cgc cag cca ggc ctc ggc cag gtt tat gat Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp 180 185 190			577
gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat Val Asn Ser Tyr Ser Leu Ala Ala Gly Arg Glu Ala Gly Ala Asp 195 200 205			625
gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu 210 215 220			673
atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly 225 230 235 240			721
gct gtt ggc ggt gct ggt tca gct ggc gtg cgc cag gtt ctc aac gag Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu 245 250 255			769
cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val 260 265 270			817
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu 275 280 285			865
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg 290 295 300			913
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val 305 310 315 320			961
ggt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa 1009 Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys 325 330 335			
ggg ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac 1057 Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr 340 345 350			

215	220	225	
tct gag act gca ttg agg gag acg ctc gat aag cct gca gag gtt gcg			835
Ser Glu Thr Ala Leu Arg Glu Thr Leu Asp Lys Pro Ala Glu Val Ala			
230	235	240	245
gat gtg atc atc act gtg ggt ggg atc tcg gcg ggc gcg ttc gat gtg			883
Asp Val Ile Ile Thr Val Gly Gly Ile Ser Ala Gly Ala Phe Asp Val			
	250	255	260
gtc aaa gcc gtg gga act aag act ggt ggt ttt gaa ttc ttc ccc att			931
Val Lys Ala Val Gly Thr Lys Thr Gly Gly Phe Glu Phe Phe Pro Ile			
	265	270	275
gcg atg aag ccg ggt aaa ccg caa ggt cat ggg cag tgg ggc gac gca			979
Ala Met Lys Pro Gly Lys Pro Gln Gly His Gly Gln Trp Gly Asp Ala			
	280	285	290
aaa gtg gtg tgt ctg ccg gga aac ccg gtg gcg gcg tgg gtt agt ttt			
1027			
Lys Val Val Cys Leu Pro Gly Asn Pro Val Ala Ala Trp Val Ser Phe			
	295	300	305
agg ctc ttt gtt gtt ccg gta att gag aga tta ggg ggt gga aag agg			
1075			
Arg Leu Phe Val Val Pro Val Ile Glu Arg Leu Gly Gly Gly Lys Arg			
	310	315	320
ctg gcg tcg ata agc gaa ctc cct gtg gtg gcg ctg cgc tcg aac ccg			
1123			
Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala Leu Arg Ser Asn Arg			
	330	335	340
gcg ctg aag gcg ccg gag ggc ccc gta ttg gcg ata ccg gtg gcg att			
1171			
Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala Ile Pro Val Ala Ile			
	345	350	355
gat tgg gag aaa aga atg gca aat tct cag gca cat cga tcc cat atg			
1219			
Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala His Arg Ser His Met			
	360	365	370
gtc ggt gca ctg gct gga agt ggc ggt att gca ctg gtg act tcg tcg			
1267			
Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala Leu Val Thr Ser Ser			
	375	380	385
att gcc gag gac ggt ctg gtt gat gtt gtg ctg ggg aga atg			
1309			
Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu Gly Arg Met			
	390	395	400
taaatagaata tcatcattct tgc			
1332			

<210> 776

<211> 403

<212> PRT

<213> Corynebacterium glutamicum

<400> 776

Val	Ala	Gln	Gln	Arg	Ser	Val	Asp	Asp	Tyr	Leu	Ser	Ile	Leu	Ile	Asp
1				5					10					15	
Ser	Val	Ala	Pro	Leu	Pro	Pro	Val	Lys	Thr	Pro	Ile	Leu	Gly	Ala	His
			20					25					30		
Pro	Leu	Ser	His	Leu	Ala	Glu	Asp	Val	Val	Ala	Thr	Ile	Pro	Ile	Pro
		35					40					45			
Lys	Phe	Thr	Asn	Ser	Ala	Val	Asp	Gly	Tyr	Ala	Ile	Leu	Lys	Glu	Asp
	50					55					60				
Ile	His	Gly	Ser	Gly	Pro	Trp	Thr	Phe	Leu	Val	Gly	Gly	Asp	Thr	Pro
65					70					75					80
Ala	Gly	Ser	Ala	Pro	Ala	Ser	Ile	Asn	Asn	Gly	Lys	Ala	Ile	Arg	Val
				85					90					95	
Met	Thr	Gly	Gly	Pro	Val	Pro	Ser	Thr	Asn	Lys	Asp	Met	Ile	Val	Val
			100					105					110		
Pro	Val	Glu	Leu	Thr	Asn	Ala	Pro	Val	Asp	His	Ser	Leu	Pro	Thr	Glu
		115					120					125			
Ile	Thr	Ile	Asn	Glu	Leu	Pro	Gly	Glu	Arg	Asn	Asn	Ile	Arg	His	Ala
	130					135					140				
Gly	Glu	His	Leu	Lys	Glu	Gly	Glu	Ile	Ala	Val	Ala	Ala	Gly	Thr	Ala
145					150					155					160
Phe	Asp	Ala	Gly	Thr	Val	Ser	Thr	Val	Ile	Ser	Val	Gly	His	Asp	Thr
				165					170					175	
Val	Lys	Ala	His	Pro	Cys	Pro	Arg	Val	Ala	Val	Ile	Thr	Thr	Gly	Asp
			180					185						190	
Glu	Leu	Asn	Gln	Gly	Asn	Pro	Trp	Gly	Ile	Pro	Asn	Ser	Asn	Gly	Pro
		195					200					205			
Met	Leu	Val	Ala	Glu	Leu	Lys	Arg	Val	Gly	Ile	Lys	Asp	Pro	Gln	His
	210					215					220				
Phe	His	Ser	Asp	Asp	Ser	Glu	Thr	Ala	Leu	Arg	Glu	Thr	Leu	Asp	Lys
225					230					235					240
Pro	Ala	Glu	Val	Ala	Asp	Val	Ile	Ile	Thr	Val	Gly	Gly	Ile	Ser	Ala
				245					250					255	
Gly	Ala	Phe	Asp	Val	Val	Lys	Ala	Val	Gly	Thr	Lys	Thr	Gly	Gly	Phe
			260					265					270		
Glu	Phe	Phe	Pro	Ile	Ala	Met	Lys	Pro	Gly	Lys	Pro	Gln	Gly	His	Gly
	275						280					285			
Gln	Trp	Gly	Asp	Ala	Lys	Val	Val	Cys	Leu	Pro	Gly	Asn	Pro	Val	Ala
	290					295					300				
Ala	Trp	Val	Ser	Phe	Arg	Leu	Phe	Val	Val	Pro	Val	Ile	Glu	Arg	Leu
305					310					315					320

Gly Gly Gly Lys Arg Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala
 325 330 335
 Leu Arg Ser Asn Arg Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala
 340 345 350
 Ile Pro Val Ala Ile Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala
 355 360 365
 His Arg Ser His Met Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala
 370 375 380
 Leu Val Thr Ser Ser Ile Ala Glu Asp Gly Leu Val Asp Val Val Leu
 385 390 395 400
 Gly Arg Met

<210> 777
 <211> 1237
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (2)..(1207)
 <223> RXS03223

<400> 777
 tcca gag cca gtg cgt att gct att gca gag gca ctg ggt ttg atg tgc 49
 Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys
 1 5 10 15
 gcg gaa gag gtt caa gct agt cgt gct ttg ccg ggt ttc gcg caa gca 97
 Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala
 20 25 30
 gcg att gat ggt tat gcg gtt cga gca gtc gat gtc ggc ggc gag aag 145
 Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys
 35 40 45
 tcg ttt agc cag caa ctg ccg gtt gct cct ccg gaa aaa tcc ctg ccc 193
 Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro
 50 55 60
 gtg gtg ggt gaa gta gct gcg ggt tct cag cag ccg ttg cgc ctg cag 241
 Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln
 65 70 75 80
 cct aaa caa gca gtc atg gtc cac acc ggt gcg cca ctg ccg atg ctt 289
 Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu
 85 90 95
 gcg gat gcg gtg ctg ccc atg gcg tgg tca gat cgt ggc cgc aaa cga 337
 Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg
 100 105 110
 gta acc gcg cag cga cct gtg cgc tct ggc gag ttt gtg cgc aaa gaa 385
 Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu

115	120	125	
ggc gat gac atc caa ccg gga gac atc gca gtc agc gcc ggc gcg gtc Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val 130 135 140			433
tta ggc cct gcc caa att ggt ttg ctc gca gct gtt ggt cgc tcc aaa Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys 145 150 155 160			481
gtg ttg gtg tac cca cgc cca cgc atg tcg gtt atc tcc gta ggc gct Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala 165 170 175			529
gaa ctt gtt gat att gat cgc cag cca ggc ctc ggc cag gtt tat gat Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp 180 185 190			577
gtc aat tcc tat tct ctg gct gcc gcc ggt agg gaa gcg ggc gca gat Val Asn Ser Tyr Ser Leu Ala Ala Ala Gly Arg Glu Ala Gly Ala Asp 195 200 205			625
gtg tac cgc tac ggc att gct gcc ggt gaa cct cgt cgc atc aaa gag Val Tyr Arg Tyr Gly Ile Ala Ala Gly Glu Pro Arg Arg Ile Lys Glu 210 215 220			673
atc att gaa tcc cag atg ctg cgc tcg gaa atc atc gtc atc acc gga Ile Ile Glu Ser Gln Met Leu Arg Ser Glu Ile Ile Val Ile Thr Gly 225 230 235 240			721
gct gtt ggc ggt gct ggt tca gct ggc gtg cgc cag gtt ctc aac gag Ala Val Gly Gly Ala Gly Ser Ala Gly Val Arg Gln Val Leu Asn Glu 245 250 255			769
cta ggc gat atc gac acc gaa cgc gtc gca atg cac ccc ggt tct gtc Leu Gly Asp Ile Asp Thr Glu Arg Val Ala Met His Pro Gly Ser Val 260 265 270			817
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu 275 280 285			865
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg 290 295 300			913
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val 305 310 315 320			961
ggt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa 1009 Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys 325 330 335			
ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac 1057 Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr 340 345 350			

ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg
1105

Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu
355 360 365

gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc
1153

Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val
370 375 380

aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa
1201

Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
385 390 395 400

ggt cga tagttcgatg cgtaatgcac cgtcaggtcc
1237

Gly Arg

<210> 778

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 778

Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys
1 5 10 15

Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala
20 25 30

Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys
35 40 45

Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro
50 55 60

Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln
65 70 75 80

Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu
85 90 95

Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg
100 105 110

Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu
115 120 125

Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val
130 135 140

Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys
145 150 155 160

Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala
165 170 175

Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp

180						185						190					
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp		
195						200						205					
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu		
210						215						220					
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly		
225			230						235			240					
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu		
			245						250			255					
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val		
			260						265			270					
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu		
			275			280						285					
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg		
290						295						300					
Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val		
305			310						315			320					
Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys		
			325						330			335					
Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr		
			340			345						350					
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu		
355						360						365					
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val		
370						375						380					
Thr	Glu	Ile	Arg	Pro	Gly	Asp	Val	Val	Asp	Val	Ile	Phe	Leu	Ala	Gln		
385			390						395			400					
Gly	Arg																

```
<210> 779
<211> 1229
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (1) .. (1206)
<223> FRXA01970
```

```

<400> 779
cca gag cca gtg cgt att gct att gca gag gca ctg ggt ttg atg tgc    48
Pro Glu Pro Val Arg Ile Ala Ile Ala Glu Ala Leu Gly Leu Met Cys
      1             5             10             15

```

gcg gaa gag gtt caa gct agt cgt gct ttg ccg ggt ttc gcg caa gca 96

Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala		
			20					25					30				
gcg	att	gat	ggt	tat	gcg	gtt	cga	gca	gtc	gat	gtc	ggc	ggc	gag	aag	144	
Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys		
		35					40					45					
tcg	ttt	agc	cag	caa	ctg	ccg	gtt	gct	cct	ccg	gaa	aaa	tcc	ctg	ccc	192	
Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro		
	50					55					60						
gtg	gtg	ggt	gaa	gta	gct	gcg	ggt	tct	cag	cag	ccg	ttg	cgc	ctg	cag	240	
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln		
	65				70					75					80		
cct	aaa	caa	gca	gtc	atg	gtc	cac	acc	ggc	gcg	cca	ctg	ccg	atg	ctt	288	
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu		
			85					90						95			
gcg	gat	gcg	gtg	ctg	ccc	atg	gcg	tgg	tca	gat	cgt	ggc	cgc	aaa	cga	336	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg		
			100					105					110				
gta	acc	gcg	cag	cga	cct	gtg	cgc	tct	ggc	gag	ttt	gtg	cgc	aaa	gaa	384	
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu		
		115					120					125					
ggc	gat	gac	atc	caa	ccg	gga	gac	atc	gca	gtc	agc	gcc	ggc	gcg	gtc	432	
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val		
	130					135					140						
tta	ggc	cct	gcc	caa	att	ggt	ttg	ctc	gca	gct	gtt	ggt	cgc	tcc	aaa	480	
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys		
	145				150				155						160		
gtg	ttg	gtg	tac	cca	cgc	cca	cgc	atg	tcg	gtt	atc	tcc	gta	ggc	gct	528	
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala		
			165					170						175			
gaa	ctt	gtt	gat	att	gat	cgc	cag	cca	ggc	ctc	ggc	cag	gtt	tat	gat	576	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp		
			180				185						190				
gtc	aat	tcc	tat	tct	ctg	gct	gcc	gcc	ggt	agg	gaa	gcg	ggc	gca	gat	624	
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp		
		195				200						205					
gtg	tac	cgc	tac	ggc	att	gct	gcc	ggt	gaa	cct	cgt	cgc	atc	aaa	gag	672	
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu		
	210					215					220						
atc	att	gaa	tcc	cag	atg	ctg	cgc	tcg	gaa	atc	atc	gtc	atc	acc	gga	720	
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly		
	225				230				235						240		
gct	gtt	ggc	ggt	gct	ggt	tca	gct	ggc	gtg	cgc	cag	gtt	ctc	aac	gag	768	
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu		
				245					250					255			
cta	ggc	gat	atc	gac	acc	gaa	cgc	gtc	gca	atg	cac	ccc	ggt	tct	gtc	816	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val		

260	265	270	
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg			864
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu			
275	280	285	
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc			912
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg			
290	295	300	
ccg gtc gtg cgc atg agc ctg ggc aag agc aat gcg gcg cgc cgg gtt			960
Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val			
305	310	315	320
gtt cga gct cga gcg ctc aac cac gtt gtg tct gtg gcg ggt cga aaa			
1008			
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys			
325	330	335	
ggg ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac			
1056			
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr			
340	345	350	
ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg			
1104			
Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu			
355	360	365	
gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc			
1152			
Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val			
370	375	380	
aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa			
1200			
Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln			
385	390	395	400
ggg cga tagttcgatg cgtaatgcac cgt			
1229			
Gly Arg			

<210> 780

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 780

Pro	Glu	Pro	Val	Arg	Ile	Ala	Ile	Ala	Glu	Ala	Leu	Gly	Leu	Met	Cys
1				5					10					15	

Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala
			20					25					30		

Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys
		35					40					45			

Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60					
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln
65					70					75					80
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu
				85					90					95	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg
			100					105					110		
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu
		115					120					125			
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val
	130					135					140				
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys
145					150					155					160
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala
				165					170					175	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp
			180					185					190		
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp
		195					200					205			
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu
	210					215					220				
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly
225					230					235					240
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu
				245					250					255	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val
			260					265					270		
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu
		275					280					285			
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg
		290				295					300				
Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val
305					310					315					320
Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys
				325					330					335	
Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr
			340					345					350		
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu
		355					360					365			
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val
		370				375					380				

Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
 385 390 395 400

Gly Arg

<210> 781

<211> 708

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(685)

<223> RXA02629

<400> 781

tacctcgcag agccgggagg tagaggttac tctgacgagt gagtaggttt aaaagagtta 60

atctgcātct aātcaagtāg ccaāgtatga gtgaggaaca atg agc aag gat cca 115
 Met Ser Lys Asp Pro
 1 5

ttg gga agt ctt acc gat gtt gta gac aca cga gtt ccg ctt ccg gat 163
 Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg Val Pro Leu Pro Asp
 10 15 20

gtt gaa ccg gat ccg gag ttc ctg aag gct acg gaa aaa gaa ttc cac 211
 Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr Glu Lys Glu Phe His
 25 30 35

atg gca tcc cag aag cgc gct ctt gtt gtc ctg gtg ggc gat cat gtc 259
 Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu Val Gly Asp His Val
 40 45 50

gct gag gca gat ggg act ggc cgt ttg gtt acg gag ctg ctc tta gag 307
 Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr Glu Leu Leu Leu Glu
 55 60 65

tct ggc ttc aac gtg gac gct gtg gtc agc gtg aag tct aag aag tct 355
 Ser Gly Phe Asn Val Asp Ala Val Val Ser Val Lys Ser Lys Lys Ser
 70 75 80 85

cag att agg caa gct att gaa acc gca gtt gtt ggc ggc gct gac ctt 403
 Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val Gly Gly Ala Asp Leu
 90 95 100

gtg ctg acc atc ggc gga gtg ggc gtt ggt cct cgg gat aaa act cct 451
 Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro Arg Asp Lys Thr Pro
 105 110 115

gag gca acc agc gct gtg ttg gac cag gac gtc cca gga atc gcg cag 499
 Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val Pro Gly Ile Ala Gln
 120 125 130

gcg ctt cgt tcc tcc ggt ttg gcc tgt ggc gcg gtg gat gca agt gtt 547
 Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala Val Asp Ala Ser Val
 135 140 145

tcc cga ggc gta gcg ggc gta tcc ggc tca acc gtg gtg gtc aac ctc 595
 Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr Val Val Val Asn Leu
 150 155 160 165

gct gag tct cgt tct gca att cgt gat ggc atg gca act ctg aca ccg 643
 Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met Ala Thr Leu Thr Pro
 170 175 180

ttg gtt gat ttt gtt gta gat cag ctt cgc act tcc gtg gtt 685
 Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr Ser Val Val
 185 190 195

tgagttggtc ggggtgtgagt aga 708

<210> 782
 <211> 195
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 782
 Met Ser Lys Asp Pro Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg
 1 5 10 15

Val Pro Leu Pro Asp Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr
 20 25 30

Glu Lys Glu Phe His Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu
 35 40 45

Val Gly Asp His Val Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr
 50 55 60

Glu Leu Leu Leu Glu Ser Gly Phe Asn Val Asp Ala Val Val Ser Val
 65 70 75 80

Lys Ser Lys Lys Ser Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val
 85 90 95

Gly Gly Ala Asp Leu Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro
 100 105 110

Arg Asp Lys Thr Pro Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val
 115 120 125

Pro Gly Ile Ala Gln Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala
 130 135 140

Val Asp Ala Ser Val Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr
 145 150 155 160

Val Val Val Asn Leu Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met
 165 170 175

Ala Thr Leu Thr Pro Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr
 180 185 190

Ser Val Val
 195

```
<210> 783
<211> 402
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101) .. (379)  
<223> RXA02318
```

<400> 783																
gatatacgcc acggtaccgc gtacaaaatc ccgaatatga tcatggccaa aggagggtcag																60
cagtaagcgc atgtgcgcca ttttaaggca agatggggcc atg aat tcg ctt ttc																115
Met Asn Ser Leu Phe																
1 5																
gac gtc tcc cca cac tgg tcc tcc gcc aac gcc aag ctc acc gca cat																163
Asp Val Ser Pro His Trp Ser Ser Ala Asn Ala Lys Leu Thr Ala His																
10 15 20																
ttt aac acc gga aaa ttc tcc act ggc atg aaa ttt gtc aac ctc att																211
Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys Phe Val Asn Leu Ile																
25 30 35																
gcc gac tcc gca gaa gaa gcc aac cac cac ccc gat atc ctt ctc acc																259
Ala Asp Ser Ala Glu Glu Ala Asn His His Pro Asp Ile Leu Leu Thr																
40 45 50																
tat ggt ttt gtg gaa atc acc ctc acc agc cac gat gtg ggt gag ata																307
Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His Asp Val Gly Glu Ile																
55 60 65																
acc gac cgt gat gtc gcc cta gca aaa gtc atc gac gcc cac gcc aag																355
Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile Asp Ala His Ala Lys																
70 75 80 85																
acc ttg gcc att tcg gca gag gct taagggttaaa gattatgagc aac																402
Thr Leu Ala Ile Ser Ala Glu Ala																
90																

```
<210> 784
<211> 93
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 784
Met Asn Ser Leu Phe Asp Val Ser Pro His Trp Ser Ser Ala Asn Ala
 1          5          10          15

Lys Leu Thr Ala His Phe Asn Thr Gly Lys Phe Ser Thr Gly Met Lys
          20          25          30

Phe Val Asn Leu Ile Ala Asp Ser Ala Glu Glu Ala Asn His His Pro
          35          40          45

Asp Ile Leu Leu Thr Tyr Gly Phe Val Glu Ile Thr Leu Thr Ser His
 50          55          60

Asp Val Gly Glu Ile Thr Asp Arg Asp Val Ala Leu Ala Lys Val Ile

```


65	70	75	80
Asp Ala His Ala Lys Thr Leu Ala Ile Ser Ala Glu Ala			
85		90	
 <210> 785			
<211> 600			
<212> DNA			
<213> Corynebacterium glutamicum			
 <220>			
<221> CDS			
<222> (101)..(577)			
<223> RXA01517			
 <400> 785			
tccataagcc caaagcaccg atcccacgta cttttgctga cgtcgcggtg gttgcccgcac	60		
gttccaggaa atccatggct gctggaagga gcaacgccta atg cat gca gtt ttg	115		
	Met His Ala Val Leu		
	1 5		
tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg	163		
Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val			
	10 15 20		
atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca	211		
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser			
	25 30 35		
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg	259		
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val			
	40 45 50		
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc	307		
Leu Val Val Glu Val Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly			
	55 60 65		
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg	355		
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly			
	70 75 80 85		
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa	403		
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu			
	90 95 100		
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct	451		
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala			
	105 110 115		
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat	499		
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp			
	120 125 130		
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat	547		
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp			
	135 140 145		
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat	597		
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile			

150

155

gca

600

<210> 786

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 786

Met His Ala Val Leu Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala
 1 5 10 15

Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln
 20 25 30

Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu
 35 40 45

Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu
 50 55 60

Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg
 65 70 75 80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile
 85 90 95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu
 100 105 110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu
 115 120 125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His
 130 135 140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile
 145 150 155

<210> 787

<211> 609

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(586)

<223> RXN01304

<400> 787

atgcaggtaa acgaatttgt gcttatatca acattcgtga ttcggcaaaa ttaattaaac 60

tgaaaaaaggg gattaattac cccacttga ggagaaaattg atg ccc gca cag aac 115
 Met Pro Ala Gln Asn
 1 5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163
 Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser

	10	15	20	
gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag				211
Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln				
	25	30	35	
gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt				259
Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe				
	40	45	50	
gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc				307
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg				
	55	60	65	
gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg				355
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr				
	70	75	80	85
ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg				403
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met				
	90	95	100	
acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta				451
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu				
	105	110	115	
tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc				499
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu				
	120	125	130	
atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg				547
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly				
	135	140	145	
gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagattt				596
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu				
	150	155	160	
ttgcttatcg acg				609

<210> 788

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 788

Met	Pro	Ala	Gln	Asn	Lys	Asn	Leu	Pro	Gly	Ser	Val	Ile	Val	Val	Ser
1				5					10					15	

Asp	Arg	Ile	Lys	Ser	Gly	Glu	Arg	Ile	Asp	Lys	Ala	Gly	Pro	Val	Ala
		20						25					30		

Val	Asp	Leu	Leu	Gln	Glu	Ser	Gly	Val	Glu	Ile	Ser	Thr	Phe	Thr	Val
		35					40					45			

Val	Glu	Glu	Gly	Phe	Glu	Pro	Val	His	Gln	Glu	Leu	Val	Lys	Ala	Leu
	50					55					60				

Ala	Arg	Arg	Asp	Arg	Val	Ile	Ile	Thr	Ile	Gly	Gly	Thr	Gly	Val	Gly
65					70					75					80

[illegible]

```
<210> 789
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101) .. (1258)
<223> RXS02556
```

<400> 789																					
tgccatcata	ttaaggccaa	attgcttgga	tcctgggatt	tatttaatta	gattaaatcc										60						
gtagaaatta				gcccatagaag				catggaaagg				cgaaaacccc				ttg	atc	ggt	tcc	acc	115
																Leu	Ile	Val	Ser	Thr	5
																1					
cag	ccc	att	act	gat	cgc	agc	gca	ctc	tcg	gca	gaa	cac	gca	gag	gtg	163					
Gln	Pro	Ile	Thr	Asp	Arg	Ser	Ala	Leu	Ser	Ala	Glu	His	Ala	Glu	Val						
				10								15				20					
atc	aaa	gca	acg	ctt	cct	ctc	gtg	ggc	ggc	aag	att	aat	gag	atc	acg	211					
Ile	Lys	Ala	Thr	Leu	Pro	Leu	Val	Gly	Gly	Lys	Ile	Asn	Glu	Ile	Thr						
				25								30				35					
ccg	gtt	ttc	tac	aac	aag	atg	ttt	gcg	gct	cac	cca	gaa	ttg	atc	gct	259					
Pro	Val	Phe	Tyr	Asn	Lys	Met	Phe	Ala	Ala	His	Pro	Glu	Leu	Ile	Ala						
				40								45				50					
aac	acc	ttc	aac	cgt	ggc	aat	cag	aag	caa	ggc	gat	cag	cag	aag	gcg	307					
Asn	Thr	Phe	Asn	Arg	Gly	Asn	Gln	Lys	Gln	Gly	Asp	Gln	Gln	Lys	Ala						
				55								60				65					
ctg	gcg	gct	tcg	att	gca	acg	ttt	gcc	acc	atg	ctc	gtt	act	cct	gat	355					
Leu	Ala	Ala	Ser	Ile	Ala	Thr	Phe	Ala	Thr	Met	Leu	Val	Thr	Pro	Asp						
				70								75				80				85	
gct	cct	gac	cca	gtt	cag	ctg	ctg	tcc	cgc	att	ggc	cac	aag	cac	gtg	403					
Ala	Pro	Asp	Pro	Val	Gln	Leu	Leu	Ser	Arg	Ile	Gly	His	Lys	His	Val						
				90								95				100					

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451
 Ser Leu Gly Il Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu
 105 110 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499
 Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro
 120 125 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg 547
 Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu
 135 140 145

atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc 595
 Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly
 150 155 160 165

gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca 643
 Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala
 170 175 180

acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca 691
 Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro
 185 190 195

ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag 739
 Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln
 200 205 210

ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att 787
 Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile
 215 220 225

gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta 835
 Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val
 230 235 240 245

tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt 883
 Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val
 250 255 260

ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc 931
 Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly
 265 270 275

tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac 979
 Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp
 280 285 290

gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg
 1027
 Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val
 295 300 305

gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa
 1075
 Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu
 310 315 320 325

atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att
 1123
 Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile

330 335 340
 cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag
 1171
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys
 345 350 355
 aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta
 1219
 Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val
 360 365 370
 aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca
 1268
 Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser
 375 380 385
 ccccgaaact tcc
 1281
 <210> 790
 <211> 386
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 790
 Leu Ile Val Ser Thr Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala
 1 5 10 15
 Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys
 20 25 30
 Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His
 35 40 45
 Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly
 50 55 60
 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95
 Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
 100 105 110
 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175
 Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu

180	185	190
Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp 195 200 205		
Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp 210 215 220		
Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe 225 230 235 240		
Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala 245 250 255		
Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile 260 265 270		
Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met 275 280 285		
Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser 290 295 300		
Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro 305 310 315 320		
Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu 325 330 335		
Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly 340 345 350		
Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu 355 360 365		
Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu 370 375 380		
Ile Ser 385		

<210> 791

<211> 990

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(967)

<223> RXS02560

<400> 791

ttggggcaag ccagctaacg catttcttgt ggaaaccgca gacattgagg ccgcccacgc 60

ggaacttcta agagcagtgg aatgaaataa tccggtgctg atg cag ggc aac tcg	115
Met Gln Gly Asn Ser	
1 5	

ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca	163
Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro	

10										15										20									
gga	gaa	ctt	tta	gcc	gcc	cgc	tac	gga	caa	cct	gca	acc	tgg	acg	cca														211
Gly	Glu	Leu	Leu	Ala	Ala	Arg	Tyr	Gly	Gln	Pro	Ala	Thr	Trp	Thr	Pro														
			25																										
ccg	cag	tgg	aat	gag	acg	ctt	gat	gtc	att	cac	cag	cat	cga	tca	gtt														259
Pro	Gln	Trp	Asn	Glu	Thr	Leu	Asp	Val	Ile	His	Gln	His	Arg	Ser	Val														
			40																										
cgc	agg	tgg	ttg	gat	aaa	ccg	gtt	gat	gat	gac	acc	atc	cgc	acc	att														307
Arg	Arg	Trp	Leu	Asp	Lys	Pro	Val	Asp	Asp	Asp	Thr	Ile	Arg	Thr	Ile														
			55																										
att	tcc	gcc	gca	caa	tcg	gct	gga	acc	tct	tcc	aat	aag	cag	gtc	att														355
Ile	Ser	Ala	Ala	Gln	Ser	Ala	Gly	Thr	Ser	Ser	Asn	Lys	Gln	Val	Ile														
			70																										
tct	gtc	atc	gtg	gtt	aaa	gat	cct	gag	ctg	agg	aaa	ggc	ctc	gcg	ggg														403
Ser	Val	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Arg	Lys	Gly	Leu	Ala	Gly														
atc	act	cgc	cag	atg	ttt	ccg	cac	ctt	gag	cag	gtt	ccc	gcg	gtg	ctg														451
Ile	Thr	Arg	Gln	Met	Phe	Pro	His	Leu	Glu	Gln	Val	Pro	Ala	Val	Leu														
			105																										
att	tgg	ttg	att	gat	tat	tcc	cga	atc	agt	gcg	gtg	gca	gcc	aga	gaa														499
Ile	Trp	Leu	Ile	Asp	Tyr	Ser	Arg	Ile	Ser	Ala	Val	Ala	Ala	Arg	Glu														
			120																										
gat	ctc	cca	aca	ggg	gct	ctt	gat	tat	ctc	gat	gag	gcc	gcg	tgg	ggg														547
Asp	Leu	Pro	Thr	Gly	Ala	Leu	Asp	Tyr	Leu	Asp	Glu	Ala	Ala	Trp	Gly														
			135																										
ttc	ctc	gac	gcc	gga	atc	gca	gct	caa	aac	gct	gca	att	gct	gcg	gag														595
Phe	Leu	Asp	Ala	Gly	Ile	Ala	Ala	Gln	Asn	Ala	Ala	Ile	Ala	Ala	Glu														
			150																										
tca	ctt	gga	ttg	gga	acg	ctc	tat	ttg	ggt	tcg	gtg	cgc	aac	gat	gcg														643
Ser	Leu	Gly	Leu	Gly	Thr	Leu	Tyr	Leu	Gly	Ser	Val	Arg	Asn	Asp	Ala														
gaa	gcc	gtg	cac	aaa	ttg	ctt	ggc	ctt	cca	cct	gag	atc	gtg	cct	gtc														691
Glu	Ala	Val	His	Lys	Leu	Leu	Gly	Leu	Pro	Pro	Glu	Ile	Val	Pro	Val														
			185																										
gtg	ggc	ttg	gaa	atg	ggg	cat	gcg	gat	ccg	cct	gaa	cct	gcc	gga	att														739
Val	Gly	Leu	Glu	Met	Gly	His	Ala	Asp	Pro	Pro	Glu	Pro	Ala	Gly	Ile														
			200																										
aaa	cct	ccc	ctg	cca	caa	gaa	gcc	att	gtt	cac	tgg	gat	acc	tac	acc														787
Lys	Pro	Pro	Leu	Pro	Gln	Glu	Ala	Ile	Val	His	Trp	Asp	Thr	Tyr	Thr														
			215																										
gag	aaa	aac	ctc	gaa	ctt	atc	gat	tcc	tac	gac	cgc	gcc	ctc	gac	act														835
Glu	Lys	Asn	Leu	Glu	Leu	Ile	Asp	Ser	Tyr	Asp	Arg	Ala	Leu	Asp	Thr														
			230																										
tac	tat	tct	cgc	tac	ggc	cag	cac	cag	ctc	tgg	tcg	aag	cag	acg	gcg														883
Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp	Ser	Lys	Gln	Thr	Ala														

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
 265 270 275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
 280 285

attatggacg cct 990

<210> 792

<211> 289

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 792

Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys
 1 5 10 15

Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
 20 25 30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp

225				230				235				240			
Arg	Ala	Leu	Asp	Thr	Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp
				245				250				255			
Ser	Lys	Gln	Thr	Ala	His	Arg	Ala	Ala	Ser	Lys	Ser	Phe	Ser	Lys	Thr
				260				265				270			
Asn	Arg	Gln	Phe	Leu	Arg	Gly	Val	Phe	Glu	Arg	Ala	Gly	Phe	Gly	Leu
				275				280				285			

Arg

```
<210> 793
<211> 1425
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1402)
<223> RXA00382
```

<400> 793																
aaaacactat tgaccacccc aatcgctgtt gagagtttgt aaagttcgac tgtcaacgag 60																
ctggattggc ttcacagatt gaattaatac aatgacgcac atg aca tcg tcc aat 115																
Met Thr Ser Ser Asn 5																
1																
acg gct cga tcc gca gag tgg ttt gaa aag gct cag aag ctc acc cct 163																
Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala Gln Lys Leu Thr Pro 20																
10 15																
ggg ggt gtg aat tct cct gtt cgc gct ttc ggt tca gtt ggc gga caa 211																
Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly Ser Val Gly Gly Gln 35																
25 30																
gcc cgt ttc atc gaa aaa gct cac ggt tca acg ctg atc gat gtg gac 259																
Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr Leu Ile Asp Val Asp 50																
40 45																
gga aat gaa tac gtt gac ctg gtc tgt tct tgg ggc ccc atg ctg atg 307																
Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp Gly Pro Met Leu Met 65																
55 60																
ggg cac gct cac cca gca gtg gtc gag gct gtg cag aag gcc gtc gtg 355																
Gly His Ala His Pro Ala Val Val Glu Ala Val Gln Lys Ala Val Val 85																
70 75 80																
gat ggt ctt tct ttc ggc gct ccc acc atc ggt gag gtt gag ttg gcc 403																
Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly Glu Val Glu Leu Ala 100																
90 95																
caa gat atc gtc aag cgc act tct gtg gag gaa gtc cgc ctg gtc aac 451																
Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu Val Arg Leu Val Asn 115																
105 110																
tcc ggc act gag gcc acc atg tcg gcg gtt cgt ctg gcg cgc ggt tac 499																

Ser	Gly	Thr	Glu	Ala	Thr	Met	Ser	Ala	Val	Arg	Leu	Ala	Arg	Gly	Tyr		
		120					125					130					
act	cag	cgt	tcc	aag	att	ttg	aag	ttt	gag	ggc	tgc	tac	cac	ggc	cac	547	
Thr	Gln	Arg	Ser	Lys	Ile	Leu	Lys	Phe	Glu	Gly	Cys	Tyr	His	Gly	His		
	135					140				145							
gtc	gat	gcg	ctg	ctc	gca	tct	gct	ggc	tct	ggc	gtc	gca	act	ttc	gct	595	
Val	Asp	Ala	Leu	Leu	Ala	Ser	Ala	Gly	Ser	Gly	Val	Ala	Thr	Phe	Ala		
150					155					160					165		
ctg	cct	gat	tcc	cca	ggc	atc	acc	ggc	gct	cag	act	tct	gac	act	att	643	
Leu	Pro	Asp	Ser	Pro	Gly	Ile	Thr	Gly	Ala	Gln	Thr	Ser	Asp	Thr	Ile		
				170				175						180			
gtt	gtt	cct	tac	aac	gac	att	gaa	gcc	gtg	cgc	aac	gct	ttt	gcg	gag	691	
Val	Val	Pro	Tyr	Asn	Asp	Ile	Glu	Ala	Val	Arg	Asn	Ala	Phe	Ala	Glu		
			185				190						195				
tac	cca	ggc	gag	atc	gcc	tgc	atc	atc	gca	gag	gca	gcc	ggc	ggc	aac	739	
Tyr	Pro	Gly	Glu	Ile	Ala	Cys	Ile	Ile	Ala	Glu	Ala	Ala	Gly	Gly	Asn		
	200						205					210					
atg	ggc	acc	gtc	gct	cca	aag	gac	aac	ttt	aac	gac	aag	ctt	ctc	gcg	787	
Met	Gly	Thr	Val	Ala	Pro	Lys	Asp	Asn	Phe	Asn	Asp	Lys	Leu	Leu	Ala		
	215					220					225						
atc	gct	cac	gct	gac	ggc	gcg	ctg	ctg	atc	ctc	gat	gaa	gtc	atg	acc	835	
Ile	Ala	His	Ala	Asp	Gly	Ala	Leu	Leu	Ile	Leu	Asp	Glu	Val	Met	Thr		
230					235					240					245		
ggc	ttc	cgc	acc	tct	tac	cgt	ggc	tgg	ttc	ggc	gta	gac	aag	gtt	gcc	883	
Gly	Phe	Arg	Thr	Ser	Tyr	Arg	Gly	Trp	Phe	Gly	Val	Asp	Lys	Val	Ala		
			250					255						260			
gct	gac	ctg	gtc	acc	ttc	ggc	aag	gtc	gtc	tcc	ggc	ggc	cta	cct	gcc	931	
Ala	Asp	Leu	Val	Thr	Phe	Gly	Lys	Val	Val	Ser	Gly	Gly	Leu	Pro	Ala		
			265					270					275				
gca	gcg	ttt	ggc	ggc	aag	gct	gaa	atc	atg	aac	atg	ctg	gcc	cca	cag	979	
Ala	Ala	Phe	Gly	Gly	Lys	Ala	Glu	Ile	Met	Asn	Met	Leu	Ala	Pro	Gln		
	280						285					290					
ggc	ccc	gtc	tac	caa	gca	ggc	aca	ctg	tcc	ggc	aac	ccg	gtt	gcg	gtc		
1027																	
Gly	Pro	Val	Tyr	Gln	Ala	Gly	Thr	Leu	Ser	Gly	Asn	Pro	Val	Ala	Val		
	295					300					305						
gca	gct	ggc	cgg	gca	tcg	ctt	aag	ctt	gcc	gac	gaa	tcc	ctc	tac	aca		
1075																	
Ala	Ala	Gly	Arg	Ala	Ser	Leu	Lys	Leu	Ala	Asp	Glu	Ser	Leu	Tyr	Thr		
310					315					320					325		
acc	atc	aac	gcc	aac	gca	gat	cgt	ctc	cac	ggc	ttg	atc	tct	gat	gcc		
1123																	
Thr	Ile	Asn	Ala	Asn	Ala	Asp	Arg	Leu	His	Gly	Leu	Ile	Ser	Asp	Ala		
				330					335					340			
tta	acc	cac	gaa	ggc	gta	gcc	cac	cac	att	cag	cgt	gcc	tca	aac	atg		
1171																	
Leu	Thr	His	Glu	Gly	Val	Ala	His	His	Ile	Gln	Arg	Ala	Ser	Asn	Met		

345 350 355
 ctg tct atc cgt ttt gca gaa ggt gag ggc cac aac ttc tct gat atg
 1219
 Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His Asn Phe Ser Asp Met
 360 365 370
 aag gca gcc gac atc ttc cgc ttc gca ccg ttc ttc cac act ttg ctg
 1267
 Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe Phe His Thr Leu Leu
 375 380 385
 gac aac ggc gtc tac gca cca cca agc gtt ttc gaa acc tgg ttt gtg
 1315
 Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe Glu Thr Trp Phe Val
 390 395 400 405
 tct tcc gct ctc acg gac gat gat ttc tcc aag atc gag cag gca ctc
 1363
 Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys Ile Glu Gln Ala Leu
 410 415 420
 aag ccc gcc gca cgt gca gca gca gaa gcg aag gca tca tgacgcaaac
 1412
 Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys Ala Ser
 425 430
 cattgtccat cta
 1425

<210> 794

<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 794

Met Thr Ser Ser Asn Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala
 1 5 10 15
 Gln Lys Leu Thr Pro Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly
 20 25 30
 Ser Val Gly Gly Gln Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr
 35 40 45
 Leu Ile Asp Val Asp Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp
 50 55 60
 Gly Pro Met Leu Met Gly His Ala His Pro Ala Val Val Glu Ala Val
 65 70 75 80
 Gln Lys Ala Val Val Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly
 85 90 95
 Glu Val Glu Leu Ala Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu
 100 105 110
 Val Arg Leu Val Asn Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg
 115 120 125

Leu Ala Arg Gly Tyr Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly
 130 135 140
 Cys Tyr His Gly His Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly
 145 150 155 160
 Val Ala Thr Phe Ala Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln
 165 170 175
 Thr Ser Asp Thr Ile Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg
 180 185 190
 Asn Ala Phe Ala Glu Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu
 195 200 205
 Ala Ala Gly Gly Asn Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn
 210 215 220
 Asp Lys Leu Leu Ala Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu
 225 230 235 240
 Asp Glu Val Met Thr Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly
 245 250 255
 Val Asp Lys Val Ala Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser
 260 265 270
 Gly Gly Leu Pro Ala Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn
 275 280 285
 Met Leu Ala Pro Gln Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly
 290 295 300
 Asn Pro Val Ala Val Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp
 305 310 315 320
 Glu Ser Leu Tyr Thr Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly
 325 330 335
 Leu Ile Ser Asp Ala Leu Thr His Glu Gly Val Ala His His Ile Gln
 340 345 350
 Arg Ala Ser Asn Met Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His
 355 360 365
 Asn Phe Ser Asp Met Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe
 370 375 380
 Phe His Thr Leu Leu Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe
 385 390 395 400
 Glu Thr Trp Phe Val Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys
 405 410 415
 Ile Glu Gln Ala Leu Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys
 420 425 430
 Ala Ser

<210> 795
 <211> 1233
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1210)
 <223> RXA00156

<400> 795
 accgagagcg tggtagcct catttagttt cctcctatga atcttgatgt gggtcatgcg 60

tttttatgca atatcaacca aaagttggta cgatcctcat atg aat gaa cgc aca 115
 Met Asn Glu Arg Thr
 1 5

tcg gat gca ttt gac gcc ctc ctt gtg ctc tcc ttc ggt ggt ccc gaa 163
 Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser Phe Gly Gly Pro Glu
 10 15 20

ggg cac gag gag gtt cgt ccg ttt ttg gag aat gtc act cac gga agg 211
 Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn Val Thr His Gly Arg
 25 30 35

ggg att ccg ccg gaa cgt cta gat gaa gtg gcg gtt cat tac cac cac 259
 Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala Val His Tyr His His
 40 45 50

ttc ggt ggt atc agc ccc atc aat gcg ctg aac agg gaa att atc gcc 307
 Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn Arg Glu Ile Ile Ala
 55 60 65

aat gtg gaa aaa gaa ttg gcg tct cgc gat cac aag ctg cct gtt tat 355
 Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His Lys Leu Pro Val Tyr
 70 75 80 85

ttt ggt aac cgc aac tgg aag ccg ttt gat aat gag gcc gct gaa caa 403
 Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn Glu Ala Ala Glu Gln
 90 95 100

atg gct gat gac ggc gtg aaa aac gcg ctg gtg ttg gca act tcc gct 451
 Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val Leu Ala Thr Ser Ala
 105 110 115

tgg ggt ggc tac tcc ggt tgt cgg cag tac cag gaa gat att cag ggc 499
 Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln Glu Asp Ile Gln Gly
 120 125 130

atg atc aag cac ctg gag tct cag ggg cag tcg atc acg ttc acc aag 547
 Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser Ile Thr Phe Thr Lys
 135 140 145

ctg cgt cag ttc tac gat cac cct cgt ttt gtc tcc acc atg gct caa 595
 Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val Ser Thr Met Ala Gln
 150 155 160 165

ttg gtt cag gat tcc tac gcg aag ctt ccc gat gag ctg cga gat gag 643
 Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp Glu Leu Arg Asp Glu
 170 175 180

```

gcg cgt ctg gtc ttc acc gcg cac tcc att cca ctg act gcg gac aat 691
Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro Leu Thr Ala Asp Asn
185 190 195

gct gcg gga acc cct gag gat ggc tcc ttg tat tcc aca cag gtc aag 739
Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr Ser Thr Gln Val Lys
200 205 210

gaa gcg tca gca ctg att gct gag gct gtt ggt gtg tca gat ttt gat 787
Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly Val Ser Asp Phe Asp
215 220 225

gtg gtg tgg cag tcc cgc tcg ggt agc ccg cac act ccg tgg ctg gag 835
Val Val Trp Gln Ser Arg Ser Gly Ser Pro His Thr Pro Trp Leu Glu
230 235 240 245

cct gac atc gtg gat cac gca gtg gag ctc aac gag aag ggt caa aaa 883
Pro Asp Ile Val Asp His Ala Val Glu Leu Asn Glu Lys Gly Gln Lys
250 255 260

gcg ctc gtt gtc tgc cct gta ggc ttt att tct gat cat atg gaa gtc 931
Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser Asp His Met Glu Val
265 270 275

att tgg gat ctt gat tcc gag ctg atg gaa gaa gcc gag aag cgc aac 979
Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu Ala Glu Lys Arg Asn
280 285 290

atg gtg gtc gag cgt gtc gct acc gtt ggc ccc acc gat gaa ttc gca
1027
Met Val Val Glu Arg Val Ala Thr Val Gly Pro Thr Asp Glu Phe Ala
295 300 305

gcc ctt gtg gtt gat ctc atc gag gag gca gag ctc aag cgc gtt atc
1075
Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu Leu Lys Arg Val Ile
310 315 320 325

gag cgc ctt gga aag ctg cca gca cgc gga agt tcc gtc aac ggc gca
1123
Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser Ser Val Asn Gly Ala
330 335 340

ccg tgt ggc gac ggc tgc tgt ggt acc gcc aag cat aaa acc gcg cgg
1171
Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys His Lys Thr Ala Arg
345 350 355

gtg aac ccc aac gct cgc tca gcg gcg cca gct gcc aac taggagtgat
1220
Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala Ala Asn
360 365 370

agtccctcgc aaa
1233

```

<210> 796

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 796

Met Asn Glu Arg Thr Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser
 1 5 10 15
 Phe Gly Gly Pro Glu Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn
 20 25 30
 Val Thr His Gly Arg Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala
 35 40 45
 Val His Tyr His His Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn
 50 55 60
 Arg Glu Ile Ile Ala Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His
 65 70 75 80
 Lys Leu Pro Val Tyr Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn
 85 90 95
 Glu Ala Ala Glu Gln Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val
 100 105 110
 Leu Ala Thr Ser Ala Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln
 115 120 125
 Glu Asp Ile Gln Gly Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser
 130 135 140
 Ile Thr Phe Thr Lys Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val
 145 150 155 160
 Ser Thr Met Ala Gln Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp
 165 170 175
 Glu Leu Arg Asp Glu Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro
 180 185 190
 Leu Thr Ala Asp Asn Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr
 195 200 205
 Ser Thr Gln Val Lys Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly
 210 215 220
 Val Ser Asp Phe Asp Val Val Trp Gln Ser Arg Ser Gly Ser Pro His
 225 230 235 240
 Thr Pro Trp Leu Glu Pro Asp Ile Val Asp His Ala Val Glu Leu Asn
 245 250 255
 Glu Lys Gly Gln Lys Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser
 260 265 270
 Asp His Met Glu Val Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu
 275 280 285
 Ala Glu Lys Arg Asn Met Val Val Glu Arg Val Ala Thr Val Gly Pro
 290 295 300
 Thr Asp Glu Phe Ala Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu
 305 310 315 320

Leu	Lys	Arg	Val	Ile	Glu	Arg	Leu	Gly	Lys	Leu	Pro	Ala	Arg	Gly	Ser	
				325					330							335
Ser	Val	Asn	Gly	Ala	Pro	Cys	Gly	Asp	Gly	Cys	Cys	Gly	Thr	Ala	Lys	
				340					345							350
His	Lys	Thr	Ala	Arg	Val	Asn	Pro	Asn	Ala	Arg	Ser	Ala	Ala	Pro	Ala	
				355					360							365
Ala	Asn															
		370														

```
<210> 797
<211> 810
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(787)  
<223> RXA00624
```

<400> 797																
tccatgacgt tttgaatgga aaatctccat ttgtggagtt agaagaagac cactagtttt 60																
caacaggacg acaacggccg gacatgcgac aatacaatgc atg tcc ggc cgt ctt 115																
Met Ser Gly Arg Leu 5																
1																
ctt gtt tca gtt tct agt att ttc gac cag acc cga tcg gcg gct gac 163																
Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr Arg Ser Ala Ala Asp																
10 15 20																
agg ctc att tca gac ctg cga gcc gac ggc atc gag gtc tca tta ctt 211																
Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile Glu Val Ser Leu Leu																
25 30 35																
gtc gca ccc cgc atc gat ggg gac tgg cgt ctc gcc aaa gac aaa ggg 259																
Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu Ala Lys Asp Lys Gly																
40 45 50																
acc ctc gcg tgg atg gaa caa caa cgc gaa cgc ggc cac gaa ctc atc 307																
Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg Gly His Glu Leu Ile																
55 60 65																
ctc aac ggt ttc gac caa gca gtt cag gga cgt cgc tca gaa ttc gcc 355																
Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg Arg Ser Glu Phe Ala																
70 75 80 85																
aac ctt gaa cgg cac gaa gca cgt ctt cgc ctt acc ggt gcc att agg 403																
Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu Thr Gly Ala Ile Arg																
90 95 100																
caa atg cag aaa att ggc ttc gaa ttc caa atc ttt gcc cca cct cgt 451																
Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile Phe Ala Pro Pro Arg																
105 110 115																
tgg aga atg tca gaa ggc acc ttc gcg gta ctc cca gaa ttt gat ttc 499																
Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu Pro Glu Phe Asp Phe																

120	125	130	
aac gtc gcc gcc tcg acc agg gga tta cat aac ctc gac acc ggc gaa			547
Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn Leu Asp Thr Gly Glu			
135	140	145	
ttc ttg gcg tgt aga aac ctc tcc gtg ggt gaa ggt ttt ggt gct gca			595
Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu Gly Phe Gly Ala Ala			
150	155	160	165
aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa			643
Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu			
	170	175	180
aaa gga aat aca gtg cgc ttg tcc gca tcg gcg cga aat ctc acc aac			691
Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn			
	185	190	195
cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat			739
Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala Leu Ala Leu Asp			
	200	205	210
ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc			787
Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala Ala Ala Gln Leu Ala			
	215	220	225
tagttgggga ggttcggggc acc			810

<210> 798

<211> 229

<212> PRT

<213> Corynebacterium glutamicum

<400> 798

Met Ser Gly Arg Leu Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr			
1	5	10	15
Arg Ser Ala Ala Asp Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile			
	20	25	30
Glu Val Ser Leu Leu Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu			
	35	40	45
Ala Lys Asp Lys Gly Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg			
	50	55	60
Gly His Glu Leu Ile Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg			
	65	70	75
Arg Ser Glu Phe Ala Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu			
	85	90	95
Thr Gly Ala Ile Arg Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile			
	100	105	110
Phe Ala Pro Pro Arg Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu			
	115	120	125
Pro Glu Phe Asp Phe Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn			
	130	135	140

Leu Asp Thr Gly Glu Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu
 145 150 155 160
 Gly Phe Gly Ala Ala Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val
 165 170 175
 Thr Arg Gly Ala Glu Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala
 180 185 190
 Arg Asn Leu Thr Asn Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala
 195 200 205
 Leu Ala Ala Leu Asp Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala
 210 215 220
 Ala Ala Gln Leu Ala
 225

<210> 799
 <211> 956
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(933)
 <223> RXA00306

<400> 799
 gat tcc ggc att ccc acg cag ttg gtg gag ggc agc tgg ttt gaa ccg 48
 Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15
 gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30
 gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45
 cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc 192
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60
 aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80
 gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95
 tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat 336
 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110
 gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag 384
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu

115	120	125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag			432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys			
130	135	140	
ggt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa			480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu			
145	150	155	160
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag			528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln			
165	170		175
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc			576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg			
180	185		190
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc			624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg			
195	200		205
ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat			672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp			
210	215		220
gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc			720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg			
225	230	235	240
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc			768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser			
245	250		255
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg			816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu			
260	265		270
gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac			864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn			
275	280		285
ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg			912
Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu			
290	295		300
ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag			956
Pro Ala Asp Leu Leu Asp Ser			
305	310		

<210> 800

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 800

Asp	Ser	Gly	Ile	Pro	Thr	Gln	Leu	Val	Glu	Gly	Ser	Trp	Phe	Glu	Pro
1				5					10					15	

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val

20					25					30						
Val	Gly	Pro	Pro	Glu	Ile	Gly	His	Val	Tyr	Arg	Asp	Ser	Gly	Met	Asp	
35					40					45						
Leu	Asp	Gly	Ala	Thr	Ala	Leu	Val	Val	Lys	Glu	Ala	Cys	Ala	His	Leu	
50					55					60						
Asn	Pro	Gly	Gly	Thr	Ala	His	Leu	Leu	Gly	Ala	Trp	Val	His	Ser	Ala	
65					70					75					80	
Asp	Gln	Ser	Trp	Gln	Gln	Arg	Val	Ala	Glu	Trp	Leu	Pro	Asp	Asn	Gly	
85					90					95						
Tyr	Val	Ala	Trp	Val	Ile	Glu	Arg	Asp	Ala	Val	Ser	Pro	Ala	Gln	Tyr	
100					105					110						
Val	Gly	Thr	Trp	Leu	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Arg	Ser	Pro	Glu	
115					120					125						
Ala	Ala	Ala	Arg	Thr	Thr	Ala	Trp	Leu	Asn	His	Phe	Glu	Lys	Ala	Lys	
130					135					140						
Val	Gln	Gly	Val	Gly	Phe	Gly	Phe	Ile	Ala	Ile	Gln	Arg	Leu	Glu	Glu	
145					150					155					160	
Asp	Glu	Ala	Asp	Glu	Lys	Ser	Asp	Ile	Leu	Ala	Glu	Ser	Met	Thr	Gln	
165					170					175						
Tyr	Phe	Glu	Asp	Pro	Leu	Gly	Pro	Glu	Ile	Glu	Glu	Tyr	Phe	Thr	Arg	
180					185					190						
Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg	
195					200					205						
Phe	Lys	Val	Arg	Pro	Gly	Val	Ala	Arg	Glu	Gln	Ile	Ser	Leu	Ala	Asp	
210					215					220						
Ala	Glu	Glu	Gly	Met	Gly	Phe	Ser	Pro	Val	Thr	Leu	Arg	Leu	Thr	Arg	
225					230					235					240	
Thr	Asp	Gly	Pro	Arg	Trp	Ser	His	Asp	Val	Asp	Glu	His	Val	Ala	Ser	
245					250					255						
Ile	Val	Ala	Gly	Leu	Asn	Pro	His	Gly	Leu	Pro	Phe	Glu	Glu	Ile	Leu	
260					265					270						
Glu	Met	Tyr	Ala	Met	Ala	Gln	Gly	Ile	Glu	Gly	Glu	Ser	Leu	His	Asn	
275					280					285						
Gly	Ala	Ile	Ala	Ala	Leu	Val	Asp	Leu	Ile	Arg	His	Gly	Leu	Val	Leu	
290					295					300						
Pro	Ala	Asp	Leu	Leu	Asp	Ser										
305					310											

<210> 801

<211> 1263

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1240)

<223> RXA00884

<400> 801

```

catcttccgt ttcataccct gcactctacc ctgttcttag gaattcgcta tgtttaacat 60

caattaatca tgtatagggg gcaggcacta ggcttggggc atg tca gtt ttt ggt 115
                                         Met Ser Val Phe Gly
                                         1       5

gtg tat att cat gtg ccg ttt tgt tca act cgg tgc ggt tat tgc gat 163
Val Tyr Ile His Val Pro Phe Cys Ser Thr Arg Cys Gly Tyr Cys Asp
                        10                        15                        20

ttc aac acc tat act gct ggg gaa tta ggt agt act gca ggc ccg gac 211
Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser Thr Ala Gly Pro Asp
                        25                        30                        35

acc tat ctt gac tcg ttg gaa gtt gag ttg gag atg gct gtg gct tcg 259
Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu Met Ala Val Ala Ser
                        40                        45                        50

ctg gat aat cct cgg cag gcg gaa act atc ttt att ggc ggg ggt acc 307
Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe Ile Gly Gly Gly Thr
                        55                        60                        65

ccg tcg ttg att ggt gcg gac ggt ttg gcc agg gtt ttg ggg gct gtg 355
Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg Val Leu Gly Ala Val
                        70                        75                        80                        85

cgc aat act ttt ggc att gcg gat ggt gcg gaa gtc acc acg gag tcc 403
Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu Val Thr Thr Glu Ser
                        90                        95                        100

aat ccg gag tct acc tcg cct gag ttt ttt gat ggc ctg cgt gag gcg 451
Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp Gly Leu Arg Glu Ala
                        105                        110                        115

ggc tac aac agg att tcg tta ggg atg cag tcg gcg tcg tca agc gtt 499
Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser Ala Ser Ser Ser Val
                        120                        125                        130

ttg aag gtg ctg gac cgc acg cac acc cca ggg cgc ccg gtg gcg gcg 547
Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly Arg Pro Val Ala Ala
                        135                        140                        145

gcc aag gag gca cgt gag gcg ggg ttt gag cat gtc aat ttg gac atg 595
Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His Val Asn Leu Asp Met
150                        155                        160                        165

att tat ggc acg ccg aca gag acc gat gat gat gtc cgc aag acg ctg 643
Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp Val Arg Lys Thr Leu
                        170                        175                        180

aat gcg gtg ctc gaa gcg aac gtg gat cac gtg tct gcc tat tcc ttg 691
Asn Ala Val Leu Glu Ala Asn Val Asp His Val Ser Ala Tyr Ser Leu
                        185                        190                        195

```

```

atc gtg aaa gat ggc acg gcg atg gcg cgc aag gtg cac aag ggc gag 739
Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys Val His Lys Gly Glu
      200                      205                      210

ctg cca gcg ccg gac gag gat gtc tac gct gat cgt ttt gag ctt atc 787
Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp Arg Phe Glu Leu Ile
      215                      220                      225

gac gct cgc ctg cgc tca gct ggt ttc gat tgg tac gag gtg tcc aac 835
Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp Tyr Glu Val Ser Asn
      230                      235                      240                      245

tgg gcg aaa ccc ggc gga gaa tgc aag cac aac atg ggc tat tgg gtc 883
Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn Met Gly Tyr Trp Val
      250                      255                      260

gac ggc gac tgg tgg ggc gcg ggc ccg ggc gcg cac tcg cac atc ggc 931
Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala His Ser His Ile Gly
      265                      270                      275

gac cgc cgc ttc tac aac atc aag cac cca gcg cgt tac tcc gcg cag 979
Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala Arg Tyr Ser Ala Gln
      280                      285                      290

att gcg gcc ggc gag ctg ccc att aag gaa aca gag cgg ctg acg gcg
1027
Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr Glu Arg Leu Thr Ala
      295                      300                      305

gaa gat cac cac acc gag cgc gtc atg ctt ggt ttg cgc ctg aaa caa
1075
Glu Asp His His Thr Glu Arg Val Met Leu Gly Leu Arg Leu Lys Gln
      310                      315                      320                      325

ggc gtg ccg ctg aac ctt ttc gca ccc gca gcg cgc ccg gtc atc gac
1123
Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala Arg Pro Val Ile Asp
      330                      335                      340

cgt cat atc gca ggg ggc ctg ctg cac gtc aat gcg ctg ggc aac ctg
1171
Arg His Ile Ala Gly Gly Leu Leu His Val Asn Ala Leu Gly Asn Leu
      345                      350                      355

gcg gtg acc gat gcg gga cgt ttg ctt gcc gac ggc atc atc gcc gac
1219
Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp Gly Ile Ile Ala Asp
      360                      365                      370

att ttg ctt agt gaa gaa gac taaatattta gtaggggttac aga
1263
Ile Leu Leu Ser Glu Glu Asp
      375                      380

```

<210> 802

<211> 380

<212> PRT

<213> Corynebacterium glutamicum

<400> 802

Met Ser Val Phe Gly Val Tyr Ile His Val Pro Phe Cys Ser Thr Arg
 1 5 10 15
 Cys Gly Tyr Cys Asp Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser
 20 25 30
 Thr Ala Gly Pro Asp Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu
 35 40 45
 Met Ala Val Ala Ser Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe
 50 55 60
 Ile Gly Gly Gly Thr Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg
 65 70 75 80
 Val Leu Gly Ala Val Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu
 85 90 95
 Val Thr Thr Glu Ser Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp
 100 105 110
 Gly Leu Arg Glu Ala Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser
 115 120 125
 Ala Ser Ser Ser Val Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly
 130 135 140
 Arg Pro Val Ala Ala Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His
 145 150 155 160
 Val Asn Leu Asp Met Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp
 165 170 175
 Val Arg Lys Thr Leu Asn Ala Val Leu Glu Ala Asn Val Asp His Val
 180 185 190
 Ser Ala Tyr Ser Leu Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys
 195 200 205
 Val His Lys Gly Glu Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp
 210 215 220
 Arg Phe Glu Leu Ile Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp
 225 230 235 240
 Tyr Glu Val Ser Asn Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn
 245 250 255
 Met Gly Tyr Trp Val Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala
 260 265 270
 His Ser His Ile Gly Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala
 275 280 285
 Arg Tyr Ser Ala Gln Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr
 290 295 300
 Glu Arg Leu Thr Ala Glu Asp His His Thr Glu Arg Val Met Leu Gly
 305 310 315 320
 Leu Arg Leu Lys Gln Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala

	325		330		335
Arg Pro Val Ile Asp Arg His Ile Ala Gly Gly Leu Leu His Val Asn					
	340		345		350
Ala Leu Gly Asn Leu Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp					
	355		360		365
Gly Ile Ile Ala Asp Ile Leu Leu Ser Glu Glu Asp					
	370		375		380

<210> 803

<211> 522

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(499)

<223> RXN02503

<400> 803

```

gcagcaccgg caaccacgtc cgtcaacgcg tcagaactgc cggatgcggg tatcgctcgca 60

ttcgtgaacg caccttctgc cacacaaacg agggagtaac atg acc tta aaa att 115
                                         Met Thr Leu Lys Ile
                                         1 5

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc 163
Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg
                        10 15 20

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc 211
Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr
                        25 30 35

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
                        40 45 50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
                        55 60 65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
                        70 75 80 85

ttc cac ctg gtc gtg cca act cgt gcg gac tcg cgc gag gcc ctt atc 403
Phe His Leu Val Val Pro Thr Arg Ala Asp Ser Arg Glu Ala Leu Ile
                        90 95 100

gcc cgc gac ggc ctg act ctg gct gag ctt cca gaa agg cgc aaa ggt 451
Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro Glu Arg Arg Lys Gly
                        105 110 115

ggg aac ttc cgc tcc tcg acg cat ctc cca gct caa ggc aat ccg ccc 499
Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala Gln Gly Asn Pro Pro
                        120 125 130

```

tgacctggag attctccac tgc

522

<210> 804

<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 804

Met	Thr	Leu	Lys	Ile	Gly	Thr	Arg	Gly	Ser	Lys	Leu	Ala	Thr	Thr	Gln
1				5					10					15	

Ala	Gly	Thr	Ile	Arg	Asp	Gln	Leu	Lys	His	Tyr	Gly	Arg	Asp	Ala	Glu
			20					25					30		

Leu	His	Ile	Val	Thr	Thr	Pro	Gly	Asp	Val	Asn	Met	Ser	Pro	Val	Glu
		35					40					45			

Arg	Ile	Gly	Val	Gly	Val	Phe	Thr	Gln	Ala	Leu	Arg	Asp	Val	Leu	His
	50					55					60				

Ser	Gly	Glu	Cys	Asp	Val	Ala	Val	His	Ser	Met	Lys	Asp	Leu	Pro	Thr
65					70					75					80

Ala	Thr	Asp	Pro	Arg	Phe	His	Leu	Val	Val	Pro	Thr	Arg	Ala	Asp	Ser
				85					90					95	

Arg	Glu	Ala	Leu	Ile	Ala	Arg	Asp	Gly	Leu	Thr	Leu	Ala	Glu	Leu	Pro
		100						105					110		

Glu	Arg	Arg	Lys	Gly	Gly	Asn	Phe	Arg	Ser	Ser	Thr	His	Leu	Pro	Ala
	115					120						125			

Gln	Gly	Asn	Pro	Pro
130				

<210> 805

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA02503

<400> 805

gcagcaccgg caaccacgtc cgtcaacgcg tcagaactgc cggatgcggg tatcgtcgca 60

ttcgtgaacg	caccttctgc	cacacaaacg	agggagtaac	atg	acc	tta	aaa	att	115
				Met	Thr	Leu	Lys	Ile	
				1.				5	

ggt	acc	cga	gga	tcc	aaa	ctt	gcc	acc	acc	caa	gct	ggc	acc	atc	cgc	163
Gly	Thr	Arg	Gly	Ser	Lys	Leu	Ala	Thr	Thr	Gln	Ala	Gly	Thr	Ile	Arg	
			10					15					20			

gac	cag	ctg	aaa	cac	tac	gga	cgc	gac	gct	gaa	ctg	cac	atc	gtg	acc	211
Asp	Gln	Leu	Lys	His	Tyr	Gly	Arg	Asp	Ala	Glu	Leu	His	Ile	Val	Thr	
		25					30						35			

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
 Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
 40 45 50
 gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
 Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
 55 60 65
 gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
 Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
 70 75 80 85
 ttc cac ctg gtc gtg cca act cgt gcg gac tck cgc cga ggs cct tat 403
 Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa Arg Arg Xaa Pro Tyr
 90 95 100
 cgc ccn cga cgg sct gan ttt kgg ttr agc tty caa aar gsg saa agg 451
 Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa Gln Xaa Xaa Xaa Arg
 105 110 115
 tgg gaa ctt tcc gct cct cga cgc atc tcc cag ctc aag gca atc cgc 499
 Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
 120 125 130
 cct gac ctg gag att ctc cca ctt gcg cgg aaa cat tgacaccggc 545
 Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys His
 135 140 145
 atgggcaagg tca 558

<210> 806

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 806

Met Thr Leu Lys Ile Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln
 1 5 10 15
 Ala Gly Thr Ile Arg Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu
 20 25 30
 Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu
 35 40 45
 Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His
 50 55 60
 Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr
 65 70 75 80
 Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa
 85 90 95
 Arg Arg Xaa Pro Tyr Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa
 100 105 110
 Gln Xaa Xaa Xaa Arg Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln
 115 120 125

Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys
 130 135 140

His
 145

<210> 807

<211> 1245

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1222)

<223> RXA00377

<400> 807

```

aatggcgctc gggcagggcg cgcaagtact aaccagcaat tcccaagccc aaaaaccct 60
cccatatagt tctttttact gatgcattgt cctcaattag gtg tgg ctt ctt ttc 115
                               Val Trp Leu Leu Phe
                               1 5

cta aat tgg gat aaa tgg ggc aag att gag cgc atg tct gct ctt act 163
Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg Met Ser Ala Leu Thr
                               10 15 20

att cca gct gcg cgt cgc acg cta aat aac gcg ccc att att gat gcc 211
Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala Pro Ile Ile Asp Ala
                               25 30 35

gct aat ggc aag acc ccg act cgc act ccg gtg tgg ttt atg cgc cag 259
Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val Trp Phe Met Arg Gln
                               40 45 50

gcg ggt agg tcg ttg cct gag tac aag aag gtc cgt gag gga atc agc 307
Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val Arg Glu Gly Ile Ser
                               55 60 65

atg ttg gat tcc tgt ttc atg ccg gag ttg ttg gcg gag att act ttg 355
Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu Ala Glu Ile Thr Leu
                               70 75 80 85

cag ccg gtt cgt cgt cat gat gtg gat gct gcg att ttg ttc tct gac 403
Gln Pro Val Arg Arg His Asp Val Asp Ala Ala Ile Leu Phe Ser Asp
                               90 95 100

att gtg gtg ccg ttg cgt gct gcg ggt gtt ggt gtg gaa atc gtg gcg 451
Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly Val Glu Ile Val Ala
                               105 110 115

ggt cgt gga cct gtg ttg gat gcg ccg gtg cgg agc cgt ggg gat gtg 499
Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg Ser Arg Gly Asp Val
                               120 125 130

ttg aat ctt cct att ttg gag ggc aac gtt ccg gag gtg gag cag ggt 547
Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro Glu Val Glu Gln Gly
                               135 140 145

```

att ggc atc att ttg gat gag ttg tct gat tct cag gcg ttg att ggt 595
 Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser Gln Ala Leu Ile Gly
 150 155 160 165

ttt gct ggt gcg ccg ttt acg ttg gcg agt tac ttg gtt gag ggt ggt 643
 Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr Leu Val Glu Gly Gly
 170 175 180

cct tcc aag aat cat gag aag acc aaa gca atg atg cat ggt gat cct 691
 Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met Met His Gly Asp Pro
 185 190 195

gag acg tgg cat gcg ttg atg gct cgt ttg gtg ccg acg att gtg aat 739
 Glu Thr Trp His Ala Leu Met Ala Arg Leu Val Pro Thr Ile Val Asn
 200 205 210

tct ttg aag tcg cag atc gat gcg ggt atc gat gcg gtg cag ttg ttt 787
 Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp Ala Val Gln Leu Phe
 215 220 225

gat tcg tgg gct ggg ttc ctc act gag cgt gat tac acc gag ttc gtg 835
 Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp Tyr Thr Glu Phe Val
 230 235 240 245

ttg ccg tat tcc act gag att ttg gag gaa gtg ggc aag tac cag ctg 883
 Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val Gly Lys Tyr Gln Leu
 250 255 260

cct cgt att cac ttt ggt gtg ggt act ggt gag ttg ctt ggt gcg atg 931
 Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu Leu Leu Gly Ala Met
 265 270 275

agc aag gct ggc tca gag gtc atg ggt gtg gat tgg cgg gtg ccg ttg 979
 Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp Trp Arg Val Pro Leu
 280 285 290

gat aag gct gcg gag cgt att gct gcg gta tca ggt cct aag gtg ttg
 1027
 Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser Gly Pro Lys Val Leu
 295 300 305

cag ggt aac ctc gat cct gcg ttg ttg ttt gcg ggt cgc gca cct ttg
 1075
 Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala Gly Arg Ala Pro Leu
 310 315 320 325

act aag gaa att gag cgc atc aag gca gag gct cag act gct gtt gat
 1123
 Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala Gln Thr Ala Val Asp
 330 335 340

gca ggt cat gca acg ggc cat atc ttt aac ctt ggt cat ggt gtg ctt
 1171
 Ala Gly His Ala Thr Gly His Ile Phe Asn Leu Gly His Gly Val Leu
 345 350 355

cct aat acg gtg gcg gaa gat att act gaa gcc gtc tcc atc att cat
 1219
 Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala Val Ser Ile Ile His
 360 365 370

tct taaactaaga ggagtttcat gcg
1245
Ser

<210> 808
<211> 374
<212> PRT
<213> Corynebacterium glutamicum

<400> 808
Val Trp Leu Leu Phe Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg
1 5 10 15
Met Ser Ala Leu Thr Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala
20 25 30
Pro Ile Ile Asp Ala Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val
35 40 45
Trp Phe Met Arg Gln Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val
50 55 60
Arg Glu Gly Ile Ser Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu
65 70 75 80
Ala Glu Ile Thr Leu Gln Pro Val Arg Arg His Asp Val Asp Ala Ala
85 90 95
Ile Leu Phe Ser Asp Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly
100 105 110
Val Glu Ile Val Ala Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg
115 120 125
Ser Arg Gly Asp Val Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro
130 135 140
Glu Val Glu Gln Gly Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser
145 150 155 160
Gln Ala Leu Ile Gly Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr
165 170 175
Leu Val Glu Gly Gly Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met
180 185 190
Met His Gly Asp Pro Glu Thr Trp His Ala Leu Met Ala Arg Leu Val
195 200 205
Pro Thr Ile Val Asn Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp
210 215 220
Ala Val Gln Leu Phe Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp
225 230 235 240
Tyr Thr Glu Phe Val Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val
245 250 255
Gly Lys Tyr Gln Leu Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu

260	265	270
Leu Leu Gly Ala Met Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp		
275	280	285
Trp Arg Val Pro Leu Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser		
290	295	300
Gly Pro Lys Val Leu Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala		
305	310	315
Gly Arg Ala Pro Leu Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala		
325	330	335
Gln Thr Ala Val Asp Ala Gly His Ala Thr Gly His Ile Phe Asn Leu		
340	345	350
Gly His Gly Val Leu Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala		
355	360	365
Val Ser Ile Ile His Ser		
370		

<210> 809

<211> 681

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(658)

<223> RXN02504

<400> 809

cctcgattcc acctggctcgt gccaaactcgt gcggactcgc gcgaggccct tatcgcccgc 60

gacggcctga ctctggctga gcttccagaa aggcgcaaag	gtg gga act tcc gct	115
	Val Gly Thr Ser Ala	
	1 5	

cct cga cgc atc tcc cag ctc aag gca atc cgc cct gac ctg gag att	163
Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile	
10 15 20	

ctc cca ctg cgc gga aac att gac acc ggc atg ggc aag gtc acc tcc	211
Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met Gly Lys Val Thr Ser	
25 30 35	

ggt gaa ctc gat gct gtg atg ctc gcc tac gca ggc ctc acc cgc gtc	259
Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala Gly Leu Thr Arg Val	
40 45 50	

ggc atg cag gac cgc gca acg gaa gtt ttc gac gcc gac atc atc atg	307
Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met	
55 60 65	

ccc gcc ccc gca cag ggc gca ctt gcg atc gaa tgc cgc gcc gac gac	355
Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp	
70 75 80 85	

act gaa acc gtc cgc gcg ctc aac atg ctg atg cac gcc gac acg ttt 403
 Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe
 90 95 100

gtt tcc gcg gtt gca gaa cgc acc gtg ctc aac cgc ctc gaa gct ggc 451
 Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly
 105 110 115

tgt acc gcg cct gtc gca gcg cac gcc acc ttg gac ggc tac tcc ggc 499
 Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly
 120 125 130

gac acc atg act ctc acc gcc ggc gtc tac gca ctt gac ggc tct gac 547
 Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp
 135 140 145

cag ctg gta ttc tcc gcc gaa ggt gac ggc gcc cgc cca gaa gag ctc 595
 Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu
 150 155 160 165

ggc gag ctc gtt gca caa cag ctt atc gac gcc gga gcc gcc aat ttg 643
 Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu
 170 175 180

ctc ggc gac cgc agc taattagggc ccgaaatttc cat 681
 Leu Gly Asp Arg Ser
 185

<210> 810

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 810

Val Gly Thr Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
 1 5 10 15

Pro Asp Leu Glu Ile Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met
 20 25 30

Gly Lys Val Thr Ser Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala
 35 40 45

Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp
 50 55 60

Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu
 65 70 75 80

Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met
 85 90 95

His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn
 100 105 110

Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu
 115 120 125

Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala
 130 135 140

att ggc atc att ttg gat gag ttg tct gat tct cag gcg ttg att ggt 595
 Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser Gln Ala Leu Ile Gly
 150 155 160 165

ttt gct ggt gcg ccg ttt acg ttg gcg agt tac ttg gtt gag ggt ggt 643
 Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr Leu Val Glu Gly Gly
 170 175 180

cct tcc aag aat cat gag aag acc aaa gca atg atg cat ggt gat cct 691
 Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met Met His Gly Asp Pro
 185 190 195

gag acg tgg cat gcg ttg atg gct cgt ttg gtg ccg acg att gtg aat 739
 Glu Thr Trp His Ala Leu Met Ala Arg Leu Val Pro Thr Ile Val Asn
 200 205 210

tct ttg aag tcg cag atc gat gcg ggt atc gat gcg gtg cag ttg ttt 787
 Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp Ala Val Gln Leu Phe
 215 220 225

gat tcg tgg gct ggg ttc ctc act gag cgt gat tac acc gag ttc gtg 835
 Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp Tyr Thr Glu Phe Val
 230 235 240 245

ttg ccg tat tcc act gag att ttg gag gaa gtg ggc aag tac cag ctg 883
 Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val Gly Lys Tyr Gln Leu
 250 255 260

cct cgt att cac ttt ggt gtg ggt act ggt gag ttg ctt ggt gcg atg 931
 Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu Leu Leu Gly Ala Met
 265 270 275

agc aag gct ggc tca gag gtc atg ggt gtg gat tgg cgg gtg ccg ttg 979
 Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp Trp Arg Val Pro Leu
 280 285 290

gat aag gct gcg gag cgt att gct gcg gta tca ggt cct aag gtg ttg
 1027
 Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser Gly Pro Lys Val Leu
 295 300 305

cag ggt aac ctc gat cct gcg ttg ttg ttt gcg ggt cgc gca cct ttg
 1075
 Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala Gly Arg Ala Pro Leu
 310 315 320 325

act aag gaa att gag cgc atc aag gca gag gct cag act gct gtt gat
 1123
 Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala Gln Thr Ala Val Asp
 330 335 340

gca ggt cat gca acg ggc cat atc ttt aac ctt ggt cat ggt gtg ctt
 1171
 Ala Gly His Ala Thr Gly His Ile Phe Asn Leu Gly His Gly Val Leu
 345 350 355

cct aat acg gtg gcg gaa gat att act gaa gcc gtc tcc atc att cat
 1219
 Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala Val Ser Ile Ile His
 360 365 370

tct taaactaaga ggagtttcat gcg
 1245
 Ser

<210> 808
 <211> 374
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 808
 Val Trp Leu Leu Phe Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg
 1 5 10 15
 Met Ser Ala Leu Thr Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala
 20 25 30
 Pro Ile Ile Asp Ala Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val
 35 40 45
 Trp Phe Met Arg Gln Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val
 50 55 60
 Arg Glu Gly Ile Ser Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu
 65 70 75 80
 Ala Glu Ile Thr Leu Gln Pro Val Arg Arg His Asp Val Asp Ala Ala
 85 90 95
 Ile Leu Phe Ser Asp Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly
 100 105 110
 Val Glu Ile Val Ala Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg
 115 120 125
 Ser Arg Gly Asp Val Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro
 130 135 140
 Glu Val Glu Gln Gly Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser
 145 150 155 160
 Gln Ala Leu Ile Gly Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr
 165 170 175
 Leu Val Glu Gly Gly Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met
 180 185 190
 Met His Gly Asp Pro Glu Thr Trp His Ala Leu Met Ala Arg Leu Val
 195 200 205
 Pro Thr Ile Val Asn Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp
 210 215 220
 Ala Val Gln Leu Phe Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp
 225 230 235 240
 Tyr Thr Glu Phe Val Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val
 245 250 255
 Gly Lys Tyr Gln Leu Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu

260	265	270
Leu Leu Gly Ala Met Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp		
275	280	285
Trp Arg Val Pro Leu Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser		
290	295	300
Gly Pro Lys Val Leu Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala		
305	310	315
Gly Arg Ala Pro Leu Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala		
325	330	335
Gln Thr Ala Val Asp Ala Gly His Ala Thr Gly His Ile Phe Asn Leu		
340	345	350
Gly His Gly Val Leu Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala		
355	360	365
Val Ser Ile Ile His Ser		
370		

<210> 809

<211> 681

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(658)

<223> RXN02504

<400> 809

cctcgattcc acctggctcgt gccaaactcgt gcggactcgc gcgaggccct tatcgcccg 60

gacggcctga ctctggctga gcttccagaa aggcgcaaag	gtg gga act tcc gct	115
	Val Gly Thr Ser Ala	
	1 5	

cct cga cgc atc tcc cag ctc aag gca atc cgc cct gac ctg gag att	163
Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile	
10 15 20	

ctc cca ctg cgc gga aac att gac acc ggc atg ggc aag gtc acc tcc	211
Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met Gly Lys Val Thr Ser	
25 30 35	

ggt gaa ctc gat gct gtg atg ctc gcc tac gca ggc ctc acc cgc gtc	259
Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala Gly Leu Thr Arg Val	
40 45 50	

ggc atg cag gac cgc gca acg gaa gtt ttc gac gcc gac atc atc atg	307
Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met	
55 60 65	

ccc gcc ccc gca cag ggc gca ctt gcg atc gaa tgc cgc gcc gac gac	355
Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp	
70 75 80 85	

act gaa acc gtc cgc gcg ctc aac atg ctg atg cac gcc gac acg ttt 403
 Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe
 90 95 100

gtt tcc gcg gtt gca gaa cgc acc gtg ctc aac cgc ctc gaa gct ggc 451
 Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly
 105 110 115

tgt acc gcg cct gtc gca gcg cac gcc acc ttg gac ggc tac tcc ggc 499
 Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly
 120 125 130

gac acc atg act ctc acc gcc ggc gtc tac gca ctt gac ggc tct gac 547
 Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp
 135 140 145

cag ctg gta ttc tcc gcc gaa ggt gac ggc gcc cgc cca gaa gag ctc 595
 Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu
 150 155 160 165

ggc gag ctc gtt gca caa cag ctt atc gac gcc gga gcc gcc aat ttg 643
 Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu
 170 175 180

ctc ggc gac cgc agc taattagggc ccgaaatttc cat 681
 Leu Gly Asp Arg Ser
 185

<210> 810

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 810

Val Gly Thr Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
 1 5 10 15

Pro Asp Leu Glu Ile Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met
 20 25 30

Gly Lys Val Thr Ser Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala
 35 40 45

Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp
 50 55 60

Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu
 65 70 75 80

Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met
 85 90 95

His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn
 100 105 110

Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu
 115 120 125

Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala
 130 135 140

Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala
145 150 155 160

Arg Pro Glu Glu Leu Gly Glu L u Val Ala Gln Gln Leu Ile Asp Ala
165 170 175

Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser
180 185

<210> 811

<211> 561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> FRXA02504

<400> 811

gcacatccccca gctcaaggca atccgccctg acctggagat tctcccaactt gcgcggaaac 60

attgacaccg gcacgggcaa ggacacctcc ggtgaactcg atg ctt gtg atg ctc 115
Met Leu Val Met Leu
1 5

gcc tac gca ggc ctc acc cgc gtc ggc atg cag gac cgc gca acg gaa 163
Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu
10 15 20

gtt ttc gac gcc gac atc atc atg ccc gcc ccc gca cag ggc gca ctt 211
Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu
25 30 35

gcg atc gaa tgc cgc gcc gac gac act gaa acc gtc cgc gcg ctc aac 259
Ala Ile Glu Cys Arg Ala Asp Thr Glu Thr Val Arg Ala Leu Asn
40 45 50

atg ctg atg cac gcc gac acg ttt gtt tcc gcg gtt gca gaa cgc acc 307
Met Leu Met His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr
55 60 65

gtg ctc aac cgc ctc gaa gct ggc tgt acc gcg cct gtc gca gcg cac 355
Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His
70 75 80 85

gcc acc ttg gac ggc tac tcc ggc gac acc atg act ctc acc gcc ggc 403
Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly
90 95 100

gtc tac gca ctt gac ggc tct gac cag ctg gta ttc tcc gcc gaa ggt 451
Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly
105 110 115

gac ggc gcc cgc cca gaa gag ctc ggc gag ctc gtt gca caa cag ctt 499
Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu
120 125 130

atc gac gcc gga gcc gcc aat ttg ctc ggc gac cgc agc taattagggc 548

Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser
 135 140 145

ccgaaatttc cat

561

<210> 812

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 812

Met Leu Val Met Leu Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln
 1 5 10 15

Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro
 20 25 30

Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr
 35 40 45

Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe Val Ser Ala
 50 55 60

Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala
 65 70 75 80

Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met
 85 90 95

Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val
 100 105 110

Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu
 115 120 125

Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp
 130 135 140

Arg Ser
 145

<210> 813

<211> 1449

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1426)

<223> RXN01162

<400> 813

catcgaatac gtgccctgct gaatagatga catcgcagag atctataaga gtcagtgggtt 60

gtcgggggttt cacagtcact tattctatgc aggattcacc atg tat atc gtg ggg 115
 Met Tyr Ile Val Gly
 1 5

att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163

Ile	Cys	Leu	Gln	Leu	Val	Val	Met	Ser	Gln	Pro	Met	Ser	Ala	Pro	Asp		
				10					15					20			
tcc	gct	cca	gga	aca	gag	cgc	ggt	cat	gaa	cgc	acc	cat	ttt	gcg	gta	211	
Ser	Ala	Pro	Gly	Thr	Glu	Arg	Gly	His	Glu	Arg	Thr	His	Phe	Ala	Val		
			25					30					35				
gtc	ggt	gac	tcc	cag	gat	cca	gca	cag	gca	aca	gct	cct	aga	gcg	cca	259	
Val	Gly	Asp	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Thr	Ala	Pro	Arg	Ala	Pro		
			40				45					50					
gca	gaa	tca	att	act	ttg	att	ggt	att	ggt	acc	gat	ggg	ttt	gag	ggg	307	
Ala	Glu	Ser	Ile	Thr	Leu	Ile	Gly	Ile	Gly	Thr	Asp	Gly	Phe	Glu	Gly		
	55					60					65						
ctc	gga	ctc	aag	gca	cag	caa	gca	tta	caa	cgt	gcc	tct	gtg	gtg	att	355	
Leu	Gly	Leu	Lys	Ala	Gln	Gln	Ala	Leu	Gln	Arg	Ala	Ser	Val	Val	Ile		
	70				75					80					85		
gga	tca	tgg	cgc	cag	ctc	aat	ctc	gta	cct	gat	gcc	att	aag	gca	gag	403	
Gly	Ser	Trp	Arg	Gln	Leu	Asn	Leu	Val	Pro	Asp	Ala	Ile	Lys	Ala	Glu		
				90					95					100			
cgt	cgc	cca	tgg	ccg	ggt	aat	acc	aag	cat	cct	gat	tta	gat	gcc	ttg	451	
Arg	Arg	Pro	Trp	Pro	Gly	Asn	Thr	Lys	His	Pro	Asp	Leu	Asp	Ala	Leu		
			105					110					115				
ttt	aaa	gag	ttc	ctc	ggt	cgg	cat	gtt	gct	gtt	ctg	gcc	tct	ggc	gat	499	
Phe	Lys	Glu	Phe	Leu	Gly	Arg	His	Val	Ala	Val	Leu	Ala	Ser	Gly	Asp		
		120					125					130					
cca	ctg	ttt	tac	ggc	gtg	ggc	acc	gca	atg	gtc	cat	gtg	ctg	ggg	atg	547	
Pro	Leu	Phe	Tyr	Gly	Val	Gly	Thr	Ala	Met	Val	His	Val	Leu	Gly	Met		
	135					140					145						
gat	aga	ctc	acg	gtt	att	ccg	gga	cca	tca	tcc	gcg	tcg	ctt	gct	tgc	595	
Asp	Arg	Leu	Thr	Val	Ile	Pro	Gly	Pro	Ser	Ser	Ala	Ser	Leu	Ala	Cys		
	150				155					160					165		
gcc	cgc	ttg	ggt	tgg	aca	gtc	aac	cgc	aca	cgg	gtg	gtg	tac	cta	gga	643	
Ala	Arg	Leu	Gly	Trp	Thr	Val	Asn	Arg	Thr	Arg	Val	Val	Tyr	Leu	Gly		
				170					175					180			
caa	gaa	ccc	att	gag	aca	ctc	atc	ccg	att	att	gaa	tca	ggc	gct	caa	691	
Gln	Glu	Pro	Ile	Glu	Thr	Leu	Ile	Pro	Ile	Ile	Glu	Ser	Gly	Ala	Gln		
			185					190					195				
ttc	ctc	gtc	ttg	ggt	aaa	gat	gaa	ttc	agt	aca	gct	caa	gtt	gcc	acg	739	
Phe	Leu	Val	Leu	Gly	Lys	Asp	Glu	Phe	Ser	Thr	Ala	Gln	Val	Ala	Thr		
		200					205					210					
ttg	ttg	aat	gaa	ctc	gga	ctg	ggg	gag	act	cca	ctg	act	gtg	ctc	agc	787	
Leu	Leu	Asn	Glu	Leu	Gly	Leu	Gly	Glu	Thr	Pro	Leu	Thr	Val	Leu	Ser		
		215				220					225						
gat	ttg	ggc	agt	act	gat	gag	gag	atc	acc	caa	ggc	aca	gct	tca	cat	835	
Asp	Leu	Gly	Ser	Thr	Asp	Glu	Glu	Ile	Thr	Gln	Gly	Thr	Ala	Ser	His		
	230				235					240					245		
cca	cca	gct	gca	gtg	tct	gtt	ctc	aac	gtg	att	gct	gtg	gga	gct	cgc	883	
Pro	Pro	Ala	Ala	Val	Ser	Val	Leu	Asn	Val	Ile	Ala	Val	Gly	Ala	Arg		

250	255	260	
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac			931
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp			
265	270	275	
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg			979
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met			
280	285	290	
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta			
1027			
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu			
295	300	305	
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt			
1075			
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val			
310	315	320	325
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt			
1123			
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser			
330	335	340	
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta			
1171			
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val			
345	350	355	
caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc			
1219			
Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly			
360	365	370	
cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct			
1267			
Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro			
375	380	385	
gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag			
1315			
Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys			
390	395	400	405
ctt cac aca ctc caa gaa caa cac ggc gga atc atc aaa cac atc cgc			
1363			
Leu His Thr Leu Gln Glu Gln His Gly Gly Ile Ile Lys His Ile Arg			
410	415	420	
atc gac gac aca gac gtg cac caa tgg cga gtt aca aag ccg gtg act			
1411			
Ile Asp Asp Thr Asp Val His Gln Trp Arg Val Thr Lys Pro Val Thr			
425	430	435	
cca gaa gcg gtg aat tagcatcaaa aaccaacccc atg			
1449			
Pro Glu Ala Val Asn			
440			

<210> 814
 <211> 442
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 814

```

Met Tyr Ile Val Gly Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro
  1           5           10           15

Met Ser Ala Pro Asp Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg
      20           25           30

Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
      35           40           45

Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
      50           55           60

Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
      65           70           75           80

Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
      85           90           95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro
      100          105          110

Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val
      115          120          125

Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val
      130          135          140

His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser
      145          150          155          160

Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg
      165          170          175

Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile
      180          185          190

Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr
      195          200          205

Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro
      210          215          220

Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln
      225          230          235          240

Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile
      245          250          255

Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp
      260          265          270

Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro
      275          280          285

Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu

```

290	295	300	
Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser			
305	310	315	320
Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly			
	325	330	335
Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys			
	340	345	350
Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile			
	355	360	365
Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp			
	370	375	380
Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu			
	385	390	395
Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly Ile			
	405	410	415
Ile Lys His Ile Arg Ile Asp Asp Thr Asp Val His Gln Trp Arg Val			
	420	425	430
Thr Lys Pro Val Thr Pro Glu Ala Val Asn			
	435	440	
<210> 815			
<211> 1345			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1345)			
<223> FRXA01162			
<400> 815			
catcgaatac gtgccctgct gaatagatga catcgcagag atctataaga gtcagtgggtt 60			
gtcgggggttt cacagtcact tattctatgc aggattcacc atg tat atc gtg ggg 115			
		Met Tyr Ile Val Gly	5
att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163			
Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro Met Ser Ala Pro Asp	10	15	20
tcc gct cca gga aca gag cgc ggt cat gaa cgc acc cat ttt gcg gta 211			
Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg Thr His Phe Ala Val	25	30	35
gtc ggt gac tcc cag gat cca gca cag gca aca gct cct aga gcg cca 259			
Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr Ala Pro Arg Ala Pro	40	45	50
gca gaa tca att act ttg att ggt att ggt acc gat ggg ttt gag ggg 307			
Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr Asp Gly Phe Glu Gly			

55	60	65	
ctc gga ctc aag gca cag caa gca tta caa cgt gcc tct gtg gtg att Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg Ala Ser Val Val Ile 70 75 80 85			355
gga tca tgg cgc cag ctc aat ctc gta cct gat gcc att aag gca gag Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp Ala Ile Lys Ala Glu 90 95 100			403
cgt cgc cca tgg ccg ggt aat acc aag cat cct gat tta gat gcc ttg Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro Asp Leu Asp Ala Leu 105 110 115			451
ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp 120 125 130			499
cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met 135 140 145			547
gat aga ctc acg gtt att ccg gga cca tca tcc gcg tcg ctt gct tgc Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys 150 155 160 165			595
gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly 170 175 180			643
caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln 185 190 195			691
ttc ctc gtc ttg ggt aaa gat gaa ttc agt aca gct caa gtt gcc acg Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr 200 205 210			739
ttg ttg aat gaa ctc gga ctg ggg gag act cca ctg act gtg ctc agc Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser 215 220 225			787
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His 230 235 240 245			835
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg 250 255 260			883
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp 265 270 275			931
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met 280 285 290			979
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta 1027 Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu			

295 300 305
 cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt
 1075
 Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val
 310 315 320 325
 gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt
 1123
 Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser
 330 335 340
 gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta
 1171
 Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val
 345 350 355
 caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc
 1219
 Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly
 360 365 370
 cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct
 1267
 Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro
 375 380 385
 gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag
 1315
 Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys
 390 395 400 405
 ctt cac aca ctc caa gaa caa cac ggc gga
 1345
 Leu His Thr Leu Gln Glu Gln His Gly Gly
 410 415

 <210> 816
 <211> 415
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 816
 Met Tyr Ile Val Gly Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro
 1 5 10 15
 Met Ser Ala Pro Asp Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg
 20 25 30
 Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr
 35 40 45
 Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr
 50 55 60
 Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg
 65 70 75 80
 Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp
 85 90 95

Ala Ile Lys Ala Glu Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro
 100 105 110
 Asp Leu Asp Ala Leu Phe Lys Glu Phe Leu Gly Arg His Val Ala Val
 115 120 125
 Leu Ala Ser Gly Asp Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val
 130 135 140
 His Val Leu Gly Met Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser
 145 150 155 160
 Ala Ser Leu Ala Cys Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg
 165 170 175
 Val Val Tyr Leu Gly Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile
 180 185 190
 Glu Ser Gly Ala Gln Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr
 195 200 205
 Ala Gln Val Ala Thr Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro
 210 215 220
 Leu Thr Val Leu Ser Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln
 225 230 235 240
 Gly Thr Ala Ser His Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile
 245 250 255
 Ala Val Gly Ala Arg Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp
 260 265 270
 Val Ser Asn Glu Asp Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro
 275 280 285
 Thr Gln Gly Gln Met Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu
 290 295 300
 Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser
 305 310 315 320
 Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly
 325 330 335
 Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys
 340 345 350
 Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile
 355 360 365
 Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp
 370 375 380
 Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu
 385 390 395 400
 Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly
 405 410 415

atc atg ggt gtg aaa aat gcg ggt gcg att gcc cag gcg ctc atg gac 691
 Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala Gln Ala Leu Met Asp
 185 190 195

ggc ggg ctt gat gca gat act cca gca gct gtt att cag gaa ggc act 739
 Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val Ile Gln Glu Gly Thr
 200 205 210

act gat gca caa cgc tca gtt cgg tgc acc ttg ggc aca ttg ggt gca 787
 Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu Gly Thr Leu Gly Ala
 215 220 225

gtc atg gtg gag gaa gag att aag cct cca gct gtg tat gtc att gga 835
 Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala Val Tyr Val Ile Gly
 230 235 240 245

caa gtt gct ggc ctc taagcagatc gcctaagaat ggg 873
 Gln Val Ala Gly Leu
 250

<210> 818

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 818

Met Thr Ile Ser Gln Glu Asn Gln Pro Ile Ile Gln Pro Val Ser Leu
 1 5 10 15

Ile Gly Gly Gly Pro Gly Ala Trp Asp Leu Ile Thr Val Arg Gly Met
 20 25 30

Asn Arg Leu Gln Glu Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro
 35 40 45

Thr Asp Glu Leu Glu Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val
 50 55 60

Asp Val Ser Lys Leu Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr
 65 70 75 80

Asn Glu Met Leu Val Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg
 85 90 95

Leu Lys Gly Gly Asp Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu
 100 105 110

Glu Phe Leu Gly Glu His Gly Ile Glu Cys Glu Val Ile Pro Gly Val
 115 120 125

Thr Ser Ala Val Ser Val Pro Ala Ala Ala Gly Ile Pro Ile Thr Asn
 130 135 140

Arg Gly Val Val His Ser Phe Thr Val Val Ser Gly His Leu Pro Pro
 145 150 155 160

Gly His Pro Lys Ser Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly
 165 170 175

Gly Thr Leu Ser Ile Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala
 180 185 190

Gln Ala Leu Met Asp Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val
 195 200 205

Ile Gln Glu Gly Thr Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu
 210 215 220

Gly Thr Leu Gly Ala Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala
 225 230 235 240

Val Tyr Val Ile Gly Gln Val Ala Gly Leu
 245 250

<210> 819

<211> 1917

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1894)

<223> RXN00371

<400> 819

gtcgtggaca atcccggatc gaaaatttga ttcggctttt ttcattggctg ttgatggagt 60

acgttggctcg ttttcgagac aagtactaga aaagatattg atg act atc gcc cat 115
 Met Thr Ile Ala His
 1 5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser
 10 15 20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val
 25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro
 40 45 50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu
 55 60 65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr
 70 75 80 85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403
 Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile
 90 95 100

cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc 451
 Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg
 105 110 115

atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt 499
 Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg
 120 125 130

cca gca cca cca acc gct gca gag atc acg gaa gtt tct gag gcg act 547
 Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu Val Ser Glu Ala Thr
 135 140 145

cca gct cag att gtt gag ctt gtg cag gat gct ctt tct tat ggt gga 595
 Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly
 150 155 160 165

gat gtt att cgt ctt gtc acc ggc aac cca ttg agc agc gat gcc aca 643
 Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr
 170 175 180

ctg gct gag atc tct gca gtt tcc gag gct ggc ctg gag ttc cag gtg 691
 Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val
 185 190 195

gtt cca ggt atg tct ttg cct gca acg gtt cct gca ttt gcg gga att 739
 Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly Ile
 200 205 210

gcg ttg ggt tct acc tac acc gaa act gat gtc aac ggt caa aac ttg 787
 Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu
 215 220 225

gac tgg gat cag ttg gct agc gca cct cag cct ttg gtg ctg cag gcc 835
 Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala
 230 235 240 245

cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat 883
 Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu Leu Lys Ala Arg Asn
 250 255 260

atg tct ttg gaa act cct gtt tct gtc acc gct aac ggc acc acc cgt 931
 Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala Asn Gly Thr Thr Arg
 265 270 275

ttg cag cgc acc tat gac acc act tta ggt ctg ttg cac aag ctt gat 979
 Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu Leu His Lys Leu Asp
 280 285 290

gct gaa cta agc gga cct ttg gtt gtt acc ttg ggc aag ggt gtg gat
 1027
 Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val Asp
 295 300 305

gat cgc tcc aag tac tct tgg tgg gaa aac cgc gct ctg tac ggt tgg
 1075
 Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg Ala Leu Tyr Gly Trp
 310 315 320 325

cgt gtg ctg gtg cct cgc gct cgg gag caa gcg gca tcc atg tcc gca
 1123
 Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala Ala Ser Met Ser Ala
 330 335 340

cgt ctg agc agc cac ggc gct atc ccg cag gaa gtc cct acc att tct
 1171

Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu Val Pro Thr Ile Ser
 345 350 355
 gtc gaa cca ccg cgc aac cca gcg caa atg gaa cgc gcc atc aag ggc
 1219
 Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala Ile Lys Gly
 360 365 370
 atc gtc gaa gga cgc tac cag tgg gtt gtc ctc acc agc gtc aac gca
 1267
 Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser Val Asn Ala
 375 380 385
 gtg aag gca gtc tgg gag aaa atc acc gaa ttc ggc ctc gat tca cgt
 1315
 Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe Gly Leu Asp Ser Arg
 390 395 400 405
 tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa acc gcc gct
 1363
 Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys Thr Ala Ala
 410 415 420
 gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct gca cgt acc
 1411
 Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro Ala Arg Thr
 425 430 435
 agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa tat ttc gaa
 1459
 Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu Tyr Phe Glu
 440 445 450
 gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca gat atc gca
 1507
 Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala Asp Ile Ala
 455 460 465
 acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg gaa gtc gaa
 1555
 Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp Glu Val Glu
 470 475 480 485
 gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca agc gct gat
 1603
 Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro Ser Ala Asp
 490 495 500
 atc cga gat atg atc aag acc ggc gga ttt gat gca gtt gcc ttc acc
 1651
 Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val Ala Phe Thr
 505 510 515
 tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt aaa cca cac
 1699
 Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly Lys Pro His
 520 525 530
 cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca gcg acc gct
 1747
 Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala Ala Thr Ala

535 540 545
 gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc gcc gaa gta
 1795
 Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile Ala Glu Val
 550 555 560 565

 cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat ctg cgc gct
 1843
 Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp Leu Arg Ala
 570 575 580

 aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt cga aaa gcg
 1891
 Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg Arg Lys Ala
 585 590 595

 tct taaaagggttt ttcactaggg tgt
 1917
 Ser

<210> 820
 <211> 598
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 820
 Met Thr Ile Ala His Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu
 1 5 10 15

 Thr Asn Gln Val Ser Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly
 20 25 30

 Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
 35 40 45

 Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50 55 60

 Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65 70 75 80

 Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
 85 90 95

 Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
 100 105 110

 Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
 115 120 125

 Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
 130 135 140

 Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
 145 150 155 160

 Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
 165 170 175

Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300
 Gly Lys Gly Val Asp Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg
 305 310 315 320
 Ala Leu Tyr Gly Trp Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala
 325 330 335
 Ala Ser Met Ser Ala Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu
 340 345 350
 Val Pro Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu
 355 360 365
 Arg Ala Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu
 370 375 380
 Thr Ser Val Asn Ala Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe
 385 390 395 400
 Gly Leu Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly
 405 410 415
 Glu Lys Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu
 420 425 430
 Leu Pro Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe
 435 440 445
 Pro Glu Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro
 450 455 460
 Arg Ala Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu
 465 470 475 480
 Gly Trp Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala
 485 490 495

Pro Pro Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp
500 505 510

Ala Val Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile
515 520 525

Ala Gly Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met
530 535 540

Thr Ala Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro
545 550 555 560

Glu Ile Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val
565 570 575

Ala Asp Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg
580 585 590

Arg Arg Arg Lys Ala Ser
595

<210> 821
<211> 1024
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1024)
<223> FRXA00371

<400> 821
gtcgtggaca atcccggatc gaaaatttga ttcggctttt ttcattggctg ttgatggagt 60

acgttgggtcg ttttcgagac aagtactaga aaagatattg atg act atc gcc cat 115
Met Thr Ile Ala His
1 5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163
Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser
10 15 20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211
Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val
25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259
Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro
40 45 50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307
Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu
55 60 65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355
Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr
70 75 80 85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403
Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile

90										95					100					
cct	gtg	ccg	gaa	gat	aag	ctt	cag	gct	gcg	gaa	gat	gag	tac	gag	cg	451				
Pro	Val	Pro	Glu	Asp	Lys	Leu	Gln	Ala	Ala	Glu	Asp	Glu	Tyr	Glu	Arg					
			105					110					115							
atc	tgc	att	gaa	gcg	aag	gag	aac	ggg	gca	cg	cgt	aag	cct	cct	cgt	499				
Ile	Cys	Ile	Glu	Ala	Lys	Glu	Asn	Gly	Ala	Arg	Arg	Lys	Pro	Pro	Arg					
			120				125					130								
cca	gca	cca	cca	acc	gct	gca	gag	atc	acg	gaa	gtt	tct	gag	gcg	act	547				
Pro	Ala	Pro	Pro	Thr	Ala	Ala	Glu	Ile	Thr	Glu	Val	Ser	Glu	Ala	Thr					
			135				140					145								
cca	gct	cag	att	gtt	gag	ctt	gtg	cag	gat	gct	ctt	tct	tat	ggg	gga	595				
Pro	Ala	Gln	Ile	Val	Glu	Leu	Val	Gln	Asp	Ala	Leu	Ser	Tyr	Gly	Gly					
					155					160					165					
gat	gtt	att	cgt	ctt	gtc	acc	ggc	aac	cca	ttg	agc	agc	gat	gcc	aca	643				
Asp	Val	Ile	Arg	Leu	Val	Thr	Gly	Asn	Pro	Leu	Ser	Ser	Asp	Ala	Thr					
				170					175						180					
ctg	gct	gag	atc	tct	gca	gtt	tcc	gag	gct	ggc	ctg	gag	ttc	cag	gtg	691				
Leu	Ala	Glu	Ile	Ser	Ala	Val	Ser	Glu	Ala	Gly	Leu	Glu	Phe	Gln	Val					
			185					190					195							
gtt	cca	ggg	atg	tct	ttg	cct	gca	acg	gtt	cct	gca	ttt	gcg	gga	att	739				
Val	Pro	Gly	Met	Ser	Leu	Pro	Ala	Thr	Val	Pro	Ala	Phe	Ala	Gly	Ile					
			200				205					210								
gcg	ttg	ggg	tct	acc	tac	acc	gaa	act	gat	gtc	aac	ggg	caa	aac	ttg	787				
Ala	Leu	Gly	Ser	Thr	Tyr	Thr	Glu	Thr	Asp	Val	Asn	Gly	Gln	Asn	Leu					
			215				220				225									
gac	tgg	gat	cag	ttg	gct	agc	gca	cct	cag	cct	ttg	gtg	ctg	cag	gcc	835				
Asp	Trp	Asp	Gln	Leu	Ala	Ser	Ala	Pro	Gln	Pro	Leu	Val	Leu	Gln	Ala					
					235					240					245					
cg	gtg	gat	gac	ctt	tcc	cgt	att	gca	cag	gaa	cta	aag	gcc	cg	aat	883				
Arg	Val	Asp	Asp	Leu	Ser	Arg	Ile	Ala	Gln	Glu	Leu	Lys	Ala	Arg	Asn					
				250					255					260						
atg	tct	ttg	gaa	act	cct	gtt	tct	gtc	acc	gct	aac	ggc	acc	acc	cgt	931				
Met	Ser	Leu	Glu	Thr	Pro	Val	Ser	Val	Thr	Ala	Asn	Gly	Thr	Thr	Arg					
				265				270					275							
ttg	cag	cg	acc	tat	gac	acc	act	tta	ggg	ctg	ttg	cac	aag	ctt	gat	979				
Leu	Gln	Arg	Thr	Tyr	Asp	Thr	Thr	Leu	Gly	Leu	Leu	His	Lys	Leu	Asp					
			280				285					290								
gct	gaa	cta	agc	gga	cct	ttg	gtt	gtt	acc	ttg	ggc	aag	ggg	gtg						
Ala	Glu	Leu	Ser	Gly	Pro	Leu	Val	Val	Thr	Leu	Gly	Lys	Gly	Val						
			295			300					305									

<210> 822

<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 822

Met Thr Ile Ala His Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu
 1 5 10 15
 Thr Asn Gln Val Ser Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly
 20 25 30
 Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
 35 40 45
 Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50 55 60
 Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65 70 75 80
 Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
 85 90 95
 Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
 100 105 110
 Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
 115 120 125
 Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
 130 135 140
 Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
 145 150 155 160
 Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
 165 170 175
 Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300
 Gly Lys Gly Val
 305

<210> 823
 <211> 755
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(732)
 <223> FRXA00374

<400> 823
 acc att tct gtc gaa cca ccg cgc aac cca gcg caa atg gaa cgc gcc 48
 Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala
 1 5 10 15
 atc aag ggc atc gtc gaa gga cgc tac cag tgg gtt gtc ctc aca agc 96
 Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser
 20 25 30
 gtc aac gca gtg aag gca gtc tgg aag aaa atc acc gaa ttc ggc ctc 144
 Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu
 35 40 45
 gat tca cgt tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa 192
 Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys
 50 55 60
 acc gcc gct gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct 240
 Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro
 65 70 75 80
 gca cgt acc agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa 288
 Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu
 85 90 95
 tat ttc gaa gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca 336
 Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala
 100 105 110
 gat atc gca acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg 384
 Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp
 115 120 125
 gaa gtc gaa gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca 432
 Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro
 130 135 140
 agc gct gat atc cga gat atg atc aag acc ggc gga ttt gat gca gtt 480
 Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val
 145 150 155 160
 gcc ttc acc tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt 528
 Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly
 165 170 175
 aaa cca cac cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca 576
 Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala
 180 185 190
 gcg acc gct gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc 624

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile
 195 200 205

gcc gaa gta cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat 672
 Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

ctg cgc gct aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt 720
 Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg
 225 230 235 240

cga aaa gcg tct taaaagggttt ttactaggg tgt 755
 Arg Lys Ala Ser

<210> 824

<211> 244

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 824

Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala
 1 5 10 15

Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser
 20 25 30

Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu
 35 40 45

Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys
 50 55 60

Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro
 65 70 75 80

Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu
 85 90 95

Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala
 100 105 110

Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp
 115 120 125

Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro
 130 135 140

Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val
 145 150 155 160

Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly
 165 170 175

Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala
 180 185 190

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile
 195 200 205

Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg
 225 230 235 240

Arg Lys Ala Ser

<210> 825

<211> 1467

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1444)

<223> RXN00383

<400> 825

ccātatcttt aāccttggtc atggtgtgct tcctaatacgtgtggcggaag atattactga 60

agccgtctcc atcattcatt cttaaactaa gaggagtttc atg cgt ttt gcc atc 115
 Met Arg Phe Ala Ile
 1 5

atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163
 Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys
 10 15 20

gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211
 Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile
 25 30 35

ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259
 Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile
 40 45 50

gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307
 Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe
 55 60 65

act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355
 Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys
 70 75 80 85

tct cag tat ttc gcg ggc ggt gcg ctg cat gcg ttc ccc gca ggt gga 403
 Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala Phe Pro Ala Gly Gly
 90 95 100

gtg atg ggt att cca agc aat cca cca gca ggc gcg caa gac acc gct 451
 Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly Ala Gln Asp Thr Ala
 105 110 115

ttt gat tgg act cct ggc caa gac att tct gtt ggc gcc tta gtg cgc 499
 Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val Gly Ala Leu Val Arg
 120 125 130

cgt cag tat ggc gat gag atc gtc gat act gtg gtg tct tcg ctg ctt 547
 Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val Val Ser Ser Leu Leu

135	140	145	
ggg ggc gtt tat tcc tcc acc gct gat gat ctg ggt gtg cgc gct tcc			595
Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu Gly Val Arg Ala Ser			
150	155	160	165
gtg ccg gca ctt gct gca gcc ctt gat cag ctg gct gag gcc ggc gag			643
Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu Ala Glu Ala Gly Glu			
	170	175	180
ccg gtg act ctg tca gct gcg gtc aag gcc gtg gaa gct cag cgg gaa			691
Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val Glu Ala Gln Arg Glu			
	185	190	195
gcc gca aaa aca act tca gaa acc cgc ccc gtt ttc cag acc ttc aag			739
Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val Phe Gln Thr Phe Lys			
	200	205	210
ggc gga tac gcg gag ctg tac gaa gcg ttg gca gag caa tgc ggt gca			787
Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala Glu Gln Cys Gly Ala			
	215	220	225
gat att cac ttg gat agt ttc gtt tcc gcc atc acc aaa gat ggt gaa			835
Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile Thr Lys Asp Gly Glu			
	230	235	240
ggg ttt gcc atc aag ggc ggt ggc gaa ggc acc tac gac aag gtg att			883
Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr Tyr Asp Lys Val Ile			
	250	255	260
ttg gcg gtt ccc gct cca acc gcc gct gtg ctg ctc cgc gac ttg gca			931
Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu Leu Arg Asp Leu Ala			
	265	270	275
ccg gcc gca gcg cca cat ttg cgc gca att aag ttg gct tct tca gca			979
Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys Leu Ala Ser Ser Ala			
	280	285	290
gtc gtc ggc atg cgt ttc gat tcc agc gag ggc ctg ccc gac aac tcc			
1027			
Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly Leu Pro Asp Asn Ser			
	295	300	305
ggc gtc ctg gtc gct gtt aat gag ccg ggc atc acg gcg aag gcc ttc			
1075			
Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile Thr Ala Lys Ala Phe			
	310	315	320
acg ttc tcc tca aag aag tgg cct cac ctg gag gct cgc ggg ggc gcg			
1123			
Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu Ala Arg Gly Gly Ala			
	330	335	340
ctc gtg cgc gcg tcg ttc ggc agg cta ggc gat gag gcg tcg gca cgc			
1171			
Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp Glu Ala Ser Ala Arg			
	345	350	355
atg gac gag gat ttg ctt gtc gac gcc gcc ctc gac gat ctc ctc acc			
1219			
Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu Asp Asp Leu Leu Thr			

360 365 370
 ata acc ggg ttc gac ggc cgg gct gcc gga ctg ggt gaa att ttc gtg
 1267
 Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu Gly Glu Ile Phe Val
 375 380 385
 cag cgc tgg ttc ggt ggg ctc cca gcc tat gga gtt gat cac att gct
 1315
 Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly Val Asp His Ile Ala
 390 395 400 405
 acc gtt tcg gct gcg cgt gca gag atc gca gcc gtg cct ggc gtg gaa
 1363
 Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala Val Pro Gly Val Glu
 410 415 420
 gca att ggc gcg tgg gct ggg gga gtg gga gtt ccc gca gtt atc gca
 1411
 Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val Pro Ala Val Ile Ala
 425 430 435
 gat gcc cag gca gca gta cac agg ttg ctg gga taagcaccca aaaacactat
 1464
 Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
 440 445
 tga
 1467

<210> 826
 <211> 448
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 826
 Met Arg Phe Ala Ile Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala
 1 5 10 15
 Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu
 20 25 30
 Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser
 35 40 45
 Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp
 50 55 60
 Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
 65 70 75 80
 Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala
 85 90 95
 Phe Pro Ala Gly Gly Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly
 100 105 110
 Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val
 115 120 125

Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val
 130 135 140
 Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu
 145 150 155 160
 Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp Gln Leu
 165 170 175
 Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val
 180 185 190
 Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val
 195 200 205
 Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala
 210 215 220
 Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile
 225 230 235 240
 Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr
 245 250 255
 Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu
 260 265 270
 Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys
 275 280 285
 Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly
 290 295 300
 Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile
 305 310 315 320
 Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu
 325 330 335
 Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp
 340 345 350
 Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu
 355 360 365
 Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu
 370 375 380
 Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly
 385 390 395 400
 Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala
 405 410 415
 Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val
 420 425 430
 Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
 435 440 445

```
<220>  
<221> CDS  
<222> (101)..(382)  
<223> FRXA00376
```

```
<210> 828
<211> 94
<212> PRT
<213> Corynebacterium glutamicum
```

1146

50 55 60

Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
65 70 75 80

Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu
85 90

<210> 829
<211> 1037
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (1)..(1014)
<223> FRXA00383

<400> 829

gca ggc gcg caa gac acc gct ttt gat tgg act cct ggc caa gac att	48
Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile	
1 5 10 15	
tct gtt ggc gcc tta gtg cgc cgt cag tat ggc gat gag atc gtc gat	96
Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp	
20 25 30	
act gtg gtg tct tcg ctg ctt ggt ggc gtt tat tcc tcc acc gct gat	144
Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp	
35 40 45	
gat ctg ggt gtg cgc gct tcc gtg ccg gca ctt gct gca gcc ctt gat	192
Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Leu Asp	
50 55 60	
cag ctg gct gag gcc ggc gag ccg gtg act ctg tca gct gcg gtc aag	240
Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys	
65 70 75 80	
gcc gtg gaa gct cag cgg gaa gcc gca aaa aca act tca gaa acc cgc	288
Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg	
85 90 95	
ccc gtt ttc cag acc ttc aag ggc gga tac gcg gag ctg tac gaa gcg	336
Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala	
100 105 110	
ttg gca gag caa tgc ggt gca gat att cac ttg gat agt ttc gtt tcc	384
Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser	
115 120 125	
gcc atc acc aaa gat ggt gaa ggt ttt gcc atc aag ggc ggt ggc gaa	432
Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu	
130 135 140	
ggc acc tac gac aag gtg att ttg gcg gtt ccc gct cca acc gcc gct	480
Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala	
145 150 155 160	
gtg ctg ctc cgc gac ttg gca ccg gcc gca gcg cca cat ttg cgc gca	528

Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala
 165 170 175
 att aag ttg gct tct tca gca gtc gtc ggc atg cgt ttc gat tcc agc 576
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser
 180 185 190
 gag ggc ctg ccc gac aac tcc ggc gtc ctg gtc gct gtt aat gag ccg 624
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro
 195 200 205
 ggc atc acg gcg aag gcc ttc acg ttc tcc tca aag aag tgg cct cac 672
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His
 210 215 220
 ctg gag gct cgc ggg ggc gcg ctc gtg cgc gcg tcg ttc ggc agg cta 720
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu
 225 230 235 240
 ggc gat gag gcg tcg gca cgc atg gac gag gat ttg ctt gtc gac gcc 768
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala
 245 250 255
 gcc ctc gac gat ctc ctc acc ata acc ggg ttc gac ggc cgg gct gcc 816
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala
 260 265 270
 gga ctg ggt gaa att ttc gtg cag cgc tgg ttc ggt ggg ctc cca gcc 864
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala
 275 280 285
 tat gga gtt gat cac att gct acc gtt tcg gct gcg cgt gca gag atc 912
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile
 290 295 300
 gca gcc gtg cct ggc gtg gaa gca att ggc gcg tgg gct ggg gga gtg 960
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val
 305 310 315 320
 gga gtt ccc gca gtt atc gca gat gcc cag gca gca gta cac agg ttg
 1008
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu
 325 330 335
 ctg gga taagcaccca aaaacactat tga
 1037
 Leu Gly

<210> 830

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 830

Ala Gly Ala Gln Asp Thr Ala Ph Asp Trp Thr Pro Gly Gln Asp Ile
 1 5 10 15

Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp
 20 25 30

Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp
 35 40 45
 Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp
 50 55 60
 Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys
 65 70 75 80
 Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg
 85 90 95
 Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala
 100 105 110
 Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser
 115 120 125
 Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu
 130 135 140
 Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala
 145 150 155 160
 Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala
 165 170 175
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser
 180 185 190
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro
 195 200 205
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His
 210 215 220
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu
 225 230 235 240
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala
 245 250 255
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala
 260 265 270
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala
 275 280 285
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile
 290 295 300
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val
 305 310 315 320
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu
 325 330 335
 Leu Gly

tcc gaa aac acc gac gac caa cgc caa caa ttc gcc gaa ggc gcc gtc 691
 Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe Ala Glu Gly Ala Val
 185 190 195

caa ggc agc atc atc gcc acc tac atg cac ggc ccc gca ctc gcc cga 739
 Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly Pro Ala Leu Ala Arg
 200 205 210

aac ccc caa ctc gcc gac ctc atg ctc gca aaa gca atg ggt gtc gcg 787
 Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys Ala Met Gly Val Ala
 215 220 225

ctg aaa gac ctg gag cct ttg gac atc gac gtc atc gac cgc ctc cgc 835
 Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val Ile Asp Arg Leu Arg
 230 235 240 245

gcc gaa cgc ctg gcg tagcccccttc taaaccgggt cta 873
 Ala Glu Arg Leu Ala
 250

<210> 832

<211> 250

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 832

Met Thr Thr Leu Asn Ile Gly Leu Ile Leu Pro Asp Val Leu Gly Thr
 1 5 10 15

Tyr Gly Asp Asp Gly Asn Ala Leu Val Leu Arg Gln Arg Ala Arg Met
 20 25 30

Arg Gly Ile Asn Ala Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val
 35 40 45

Pro Ser Thr Leu Asp Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala
 50 55 60

Gln Ile Leu Ala Thr Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr
 65 70 75 80

Ala Ala Ala Ala Gly Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln
 85 90 95

Val Leu Gly Asp Ser Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu
 100 105 110

Gly Leu Ile Asp Ala Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly
 115 120 125

Glu Val Glu Thr Thr Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr
 130 135 140

Glu Arg Leu Thr Gly Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly
 145 150 155 160

Pro Asp Ala Glu Pro Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr
 165 170 175

Asp	Val	Trp	Ala	Ala	Ser	Glu	Asn	Thr	Asp	Asp	Gln	Arg	Gln	Gln	Phe
			180				185						190		
Ala	Glu	Gly	Ala	Val	Gln	Gly	Ser	Ile	Ile	Ala	Thr	Tyr	Met	His	Gly
			195				200						205		
Pro	Ala	Leu	Ala	Arg	Asn	Pro	Gln	Leu	Ala	Asp	Leu	Met	Leu	Ala	Lys
			210				215						220		
Ala	Met	Gly	Val	Ala	Leu	Lys	Asp	Leu	Glu	Pro	Leu	Asp	Ile	Asp	Val
			225				230						235		
Ile	Asp	Arg	Leu	Arg	Ala	Glu	Arg	Leu	Ala						
			245						250						

```
<210> 833
<211> 1044
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1021)
<223> RXA02134
```

<400> 833																									
tgatgaacga	catgtcgaca	ttttcttccg	ccggcgctcga	tggaacccta	aacgcctctt	60																			
ccgaagcgcc																	cgagcaaaac	acggagtaac	tttctaagcg	atg	tcc	ggc	aaa	gca	115
										Met	Ser	Gly	Lys	Ala	5										
ggc ttt acc ccc gaa gat ccc gaa gac tca gac aac cgc cac ggg aac																	163								
Gly	Phe	Thr	Pro	Glu	Asp	Pro	Glu	Asp	Ser	Asp	Asn	Arg	His	Gly	Asn										
				10						15		20													
ccc ctt ttc gaa ggt atc ttt acc gca ctt aat tgg atg acc gtt ctc																	211								
Pro	Leu	Phe	Glu	Gly	Ile	Phe	Thr	Ala	Leu	Asn	Trp	Met	Thr	Val	Leu										
				25						30		35													
ccc gtc ccc ggc gca tca gtt ttt gat cgc acc acg ggc gcc cgg gta																	259								
Pro	Val	Pro	Gly	Ala	Ser	Val	Phe	Asp	Arg	Thr	Thr	Gly	Ala	Arg	Val										
			40						45		50														
atg gcc tct ttg ccc ttt gtt ggc ttc gtt ttc gga atg ttc acc gcg																	307								
Met	Ala	Ser	Leu	Pro	Phe	Val	Gly	Phe	Val	Phe	Gly	Met	Phe	Thr	Ala										
				55						60		65													
atc atc atg tgg gct atc ggc ccc att tca ggg gtg atc cac gtc gat																	355								
Ile	Ile	Met	Trp	Ala	Ile	Gly	Pro	Ile	Ser	Gly	Val	Ile	His	Val	Asp										
70						75						80		85											
gga ctt tta gtt gcc gtt ctg atc gtc gcg ttc tgg gaa ctt ctt aat																	403								
Gly	Leu	Leu	Val	Ala	Val	Leu	Ile	Val	Ala	Phe	Trp	Glu	Leu	Leu	Asn										
				90						95		100													
cgg ttt atg cac ctc gac ggc ctc gca gat gtc tcc gat gct ttg ggt																	451								
Arg	Phe	Met	His	Leu	Asp	Gly	Leu	Ala	Asp	Val	Ser	Asp	Ala	Leu	Gly										
				105						110		115													

```

tcc tac gca gcc cca cca cgc gca cga gaa atc ctt gcc gat ccc cgc 499
Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile Leu Ala Asp Pro Arg
      120                125                130

acc gga ctt ttc ggc ctc gcc acc gcc atg ctt tcc gtt ctc ctg cag 547
Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu Ser Val Leu Leu Gln
      135                140                145

gtc gct gca gtc gca tcg ctt gtc gat tca acc gtg tgg tgg atg atc 595
Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr Val Trp Trp Met Ile
      150                155                160                165

tgc ttc atc ccc gtt ctc ggc cgc atc gct gga caa gta acc gca ctg 643
Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly Gln Val Thr Ala Leu
      170                175                180

aaa aac cac aac gcc ttc tcc ccc acc ggc ttt ggc gca cta gtc atc 691
Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe Gly Ala Leu Val Ile
      185                190                195

gga acg gtg aaa ttt tgg tgg atc gcg ctg tgg ctc ttg gtt act gct 739
Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp Leu Leu Val Thr Ala
      200                205                210

gcg ttg gct ttt tgg tgc gca gaa tta att tct cca ctt tca ccg ctg 787
Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser Pro Leu Ser Pro Leu
      215                220                225

acc agt gtt aac act ccc ttt gtc gct gga cct ttc ccc gct gca atc 835
Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro Phe Pro Ala Ala Ile
      230                235                240                245

aac ccc gcc tgg ctt gga ggc tgg gtt gcg ata acc gca gtc gtg gca 883
Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile Thr Ala Val Val Ala
      250                255                260

tgt gtt ttc gca gca ctt ttc agc cgc cgc tta tca cga agt ttc ggt 931
Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu Ser Arg Ser Phe Gly
      265                270                275

gga ctc aac gga gac tgc atc ggc gca tgc att cat ctc ggg gcg tcg 979
Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile His Leu Gly Ala Ser
      280                285                290

att tct gca gtg atg ttt gct gtt gtc gcc aat gca atg gtg
1021
Ile Ser Ala Val Met Phe Ala Val Val Ala Asn Ala Met Val
      295                300                305

taaagcggtg gcgtcttttg gga
1044

```

<210> 834

<211> 307

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 834

```

Met Ser Gly Lys Ala Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp
  1              5              10              15

```

Asn Arg His Gly Asn Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn
 20 25 30
 Trp Met Thr Val Leu Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr
 35 40 45
 Thr Gly Ala Arg Val Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe
 50 55 60
 Gly Met Phe Thr Ala Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly
 65 70 75 80
 Val Ile His Val Asp Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe
 85 90 95
 Trp Glu Leu Leu Asn Arg Phe Met His Leu Asp Gly Leu Ala Asp Val
 100 105 110
 Ser Asp Ala Leu Gly Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile
 115 120 125
 Leu Ala Asp Pro Arg Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu
 130 135 140
 Ser Val Leu Leu Gln Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr
 145 150 155 160
 Val Trp Trp Met Ile Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly
 165 170 175
 Gln Val Thr Ala Leu Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe
 180 185 190
 Gly Ala Leu Val Ile Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp
 195 200 205
 Leu Leu Val Thr Ala Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser
 210 215 220
 Pro Leu Ser Pro Leu Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro
 225 230 235 240
 Phe Pro Ala Ala Ile Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile
 245 250 255
 Thr Ala Val Val Ala Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu
 260 265 270
 Ser Arg Ser Phe Gly Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile
 275 280 285
 His Leu Gly Ala Ser Ile Ser Ala Val Met Phe Ala Val Val Ala Asn
 290 295 300
 Ala Met Val
 305

<210> 835

<211> 1197

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1174)

<223> RXA02135

<400> 835

```

cgtgtcgcag cgatttgcga gaggggttgtc ttcgtgggtg ctggctctgcc actagagttg 60
aaaacgtttt aagaaaacag tcggtttgaa ggagttgtta atg gtt cca gca gag 115
                                         Met Val Pro Ala Glu
                                         1 5

ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg 163
Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr
                        10 15 20

aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag 211
Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys
                        25 30 35

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg 259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro
                        40 45 50

cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac 307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His
                        55 60 65

ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg 355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu
                        70 75 80 85

cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att 403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile
                        90 95 100

gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac 451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp
                        105 110 115

cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc 499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile
                        120 125 130

gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag 547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys
                        135 140 145

atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att 595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile
                        150 155 160 165

tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc 643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala
                        170 175 180

ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc 691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg

```

185	190	195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc			739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile			
200	205	210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc			787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala			
215	220	225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc			835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe			
230	235	240	245
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt			883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val			
250	255	260	
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc			931
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala			
265	270	275	
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc			979
Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser			
280	285	290	
gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg			
1027			
Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met			
295	300	305	
tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag			
1075			
Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys			
310	315	320	325
att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc			
1123			
Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly			
330	335	340	
gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg			
1171			
Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr			
345	350	355	
gag taacttttcta agcgatgtcc ggc			
1197			
Glu			

<210> 836

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 836

Met	Val	Pro	Ala	Glu	Leu	Phe	Ala	Arg	Val	Glu	Phe	Pro	Asp	His	Lys
1					5				10					15	

Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro
 20 25 30
 Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
 35 40 45
 Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
 50 55 60
 Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
 65 70 75 80
 Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
 85 90 95
 Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
 100 105 110
 Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
 115 120 125
 Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
 130 135 140
 Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
 145 150 155 160
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
 165 170 175
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
 180 185 190
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
 195 200 205
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
 210 215 220
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
 225 230 235 240
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
 245 250 255
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
 260 265 270
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
 275 280 285
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
 290 295 300
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
 305 310 315 320
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
 325 330 335
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala

340 345 350

Pro Glu Gln Asn Thr Glu
355

<210> 837
<211> 645
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(622)
<223> RXA02136

<400> 837
tgggttttgggt ctgggttact acgcgtattc cgcaccatt cagcctcgta agtggcgtaac 60

ccctcgtgca cgcgttgaaa ttggtgctga agtctagcgc atg cgc acg tta gtt 115
Met Arg Thr Leu Val
1 5

ctt ggc ggg gcc agg tct ggt aag tct gct ttt gca gaa tca ctt gtt 163
Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe Ala Glu Ser Leu Val
10 15 20

gga tct ggt ccc gtt ttg tat gtc gca acg gca agg cct tcg gga gat 211
Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala Arg Pro Ser Gly Asp
25 30 35

gat cct gaa ttc gcc gag cgc att gcg gtt cat gcg gag cgg cgc cca 259
Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His Ala Glu Arg Arg Pro
40 45 50

acg tct tgg gtg ttg gac gag gag ggg gac gtc gat aag ctt ctt gcc 307
Thr Ser Trp Val Leu Asp Glu Gly Asp Val Asp Lys Leu Leu Ala
55 60 65

tcg cca ccg gcc atg ccg gtg ctc gtt gat gac ctg ggc acc tgg ctc 355
Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp Leu Gly Thr Trp Leu
70 75 80 85

acg cac gcc acc gat gcg tgc gac ggt tgg gag gcg agt tcg gcg cag 403
Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu Ala Ser Ser Ala Gln
90 95 100

ctt gag gcc aag atg gat ttg ctt atc gac gcc atc ctc cac ttt cag 451
Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala Ile Leu His Phe Gln
105 110 115

ggc gaa gat ctg gta att gtt tca cct gaa gtt ggt atg gga atc gtc 499
Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val Gly Met Gly Ile Val
120 125 130

ccg gaa tat aaa tct ggg cgc ctt ttt cgt gat gcg atc ggc aca ctt 547
Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp Arg Ile Gly Thr Leu
135 140 145

aat cag cgt gtc gca gcg att tgc gag agg gtt gtc ttc gtg gtt gct 595
Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val Val Phe Val Val Ala

150	155	160	165	
ggt ctg cca cta gag ttg aaa acg ttt taagaaaaca gtcggtttga				642
Gly Leu Pro Leu	Glu Leu Lys Thr Phe			
170				

agg 645

```
<210> 838
<211> 174
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 838																
Met	Arg	Thr	Leu	Val	Leu	Gly	Gly	Ala	Arg	Ser	Gly	Lys	Ser	Ala	Phe	
1				5					10					15		
Ala	Glu	Ser	Leu	Val	Gly	Ser	Gly	Pro	Val	Leu	Tyr	Val	Ala	Thr	Ala	
			20					25					30			
Arg	Pro	Ser	Gly	Asp	Asp	Pro	Glu	Phe	Ala	Glu	Arg	Ile	Ala	Val	His	
		35					40					45				
Ala	Glu	Arg	Arg	Pro	Thr	Ser	Trp	Val	Leu	Asp	Glu	Glu	Gly	Asp	Val	
	50					55					60					
Asp	Lys	Leu	Leu	Ala	Ser	Pro	Pro	Ala	Met	Pro	Val	Leu	Val	Asp	Asp	
65					70					75					80	
Leu	Gly	Thr	Trp	Leu	Thr	His	Ala	Thr	Asp	Ala	Cys	Asp	Gly	Trp	Glu	
				85					90					95		
Ala	Ser	Ser	Ala	Gln	Leu	Glu	Ala	Lys	Met	Asp	Leu	Leu	Ile	Asp	Ala	
			100					105					110			
Ile	Leu	His	Phe	Gln	Gly	Glu	Asp	Leu	Val	Ile	Val	Ser	Pro	Glu	Val	
	115						120					125				
Gly	Met	Gly	Ile	Val	Pro	Glu	Tyr	Lys	Ser	Gly	Arg	Leu	Phe	Arg	Asp	
	130					135					140					
Arg	Ile	Gly	Thr	Leu	Asn	Gln	Arg	Val	Ala	Ala	Ile	Cys	Glu	Arg	Val	
145					150					155					160	
Val	Phe	Val	Val	Ala	Gly	Leu	Pro	Leu	Glu	Leu	Lys	Thr	Phe			
				165					170							

<210> 839
<211> 575
<212> DNA
<213> *Corynebacterium glutamicum*

```
<220>  
<221> CDS  
<222> (1)..(552)  
<223> RXN03114
```

<400> 839
act ccg ggg cat ttt gtt gcg ctc gcg cgg gag att gcg ggc gcg gtg 48

Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val
 1 5 10 15
 cgc cgc gag ttg acg gtg ggg ttg gat gct ggt gac ggt ccg att tta 96
 Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu
 20 25 30
 agg cag agc ttt gat gtt ggt ttt ttg ctt gtc gac gcc tcc ttc cac 144
 Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His
 35 40 45
 att cat atc aat ggc gtg tct act ggg cag tcg gtt gcg ccg gat gat 192
 Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp
 50 55 60
 gta gtt gag gtg gtg cgt ggt ttg gct gat gct tcg gag ttg tcc gtg 240
 Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val
 65 70 75 80
 gaa agt gtt gct gag ttg tgt act ccc gtg gca ccg gtt tca tta tct 288
 Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser
 85 90 95
 gag gca cag ggg aat cct gcg cct att ggg tgg ttg gag cat gat ggc 336
 Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly
 100 105 110
 gtg gtg tcg ttg ggt gcg ggt att cca ggg ggg cgg gtg gag gct cgt 384
 Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg
 115 120 125
 tta gcg cgt ttt att gcg gtg att gag gcg gag acc act att acc cca 432
 Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro
 130 135 140
 tgg aat tcg ttg atc att cat gat ttg tat gag ggt gtt gca gaa cag 480
 Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln
 145 150 155 160
 gtg gtg aag gtt ctg gct ccc atg ggg ttg gtt ttt gat gct aat tca 528
 Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser
 165 170 175
 ccg ctt ctg gag tca ccg gct ttg taactcgcca ttggtgcacg tct 575
 Pro Leu Leu Glu Ser Pro Ala Leu
 180

<210> 840

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 840

Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val
 1 5 10 15
 Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu
 20 25 30
 Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His

35 40 45
 Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp
 50 55 60
 Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val
 65 70 75 80
 Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser
 85 90 95
 Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly
 100 105 110
 Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg
 115 120 125
 Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro
 130 135 140
 Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln
 145 150 155 160
 Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser
 165 170 175
 Pro Leu Leu Glu Ser Pro Ala Leu
 180

<210> 841
 <211> 1200
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1177)
 <223> RXN01810

<400> 841
 ccaccaccac aatgttgctc atcctcgcg cggttcgttgt cgcagggtggc tccatgactc 60
 gcttcaccgt cggcaacccg actggaaaat aaggcttcac atg aat aac gct ttt 115
 Met Asn Asn Ala Phe
 1 5
 cga cgc acc ctt aca tcc gta gtc ctc gcc gct agc ttg gcc tta acg 163
 Arg Arg Thr Leu Thr Ser Val Val Leu Ala Ala Ser Leu Ala Leu Thr
 10 15 20
 gcc tgc gca agc tgg gat tca cct acg gca tct tcc aat ggt gat ctg 211
 Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser Ser Asn Gly Asp Leu
 25 30 35
 att gag gag atc cag gca agc tcc acc tca aca gat ccg cgc acc ttc 259
 Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr Asp Pro Arg Thr Phe
 40 45 50
 aca ggc ttg agc atc gtg gaa gat atc ggc gat gtg gtt ccc gta acc 307
 Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp Val Val Pro Val Thr

55	60	65	
gac aac gcc tca cca gct ctg cca gtt tct ttg acc gac gct gat ggc			355
Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu Thr Asp Ala Asp Gly			
70	75	80	85
aac gac gtg gtg gtg gag aac gtg tcc cgc atc ctc cca ctg gat ctc			403
Asn Asp Val Val Val Glu Asn Val Ser Arg Ile Leu Pro Leu Asp Leu			
	90	95	100
tac gga acc tat tcc aaa acc atc gct ggc ctg gga ctc gtg gac aat			451
Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu Gly Leu Val Asp Asn			
	105	110	115
att gtg ggt cgt act gtt agt tcc acc gag cct gca ttg gcg gac att			499
Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro Ala Leu Ala Asp Ile			
	120	125	130
gag gtg gtc acc act ggc gga cac acc ctc aat gct gaa gcg atc ctt			547
Glu Val Val Thr Thr Gly Glu His Thr Leu Asn Ala Glu Ala Ile Leu			
	135	140	145
aat tta cat ccg act ttg gtg atc atc gac cac tcg atc ggc cca cgc			595
Asn Leu His Pro Thr Leu Val Ile Ile Asp His Ser Ile Gly Pro Arg			
	150	155	160
gaa gtc atc gat cag atc cgc gca gct ggt gtc gcc acg gtg atc atg			643
Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val Ala Thr Val Ile Met			
	170	175	180
tcg ccg cag cgt tcc att gcc tca att ggc gac gac atc cgc gac atc			691
Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp Asp Ile Arg Asp Ile			
	185	190	195
gcc tcc gtc gtt gga ctt cct gaa gaa ggg gag aag ctc gcg gaa cgt			739
Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu Lys Leu Ala Glu Arg			
	200	205	210
tcc gtt gct gaa gtc gaa gag gcc agc acg gtt gtc gat gaa ctc acc			787
Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val Val Asp Glu Leu Thr			
	215	220	225
cca gaa gat ccc ctc aaa atg gta ttc ctc tat gcc cgc gga act ggt			835
Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr Ala Arg Gly Thr Gly			
	230	235	240
gga gtg ttc ttc att ttg ggc gat gcc tat ggt gga cgc gat ctc att			883
Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly Gly Arg Asp Leu Ile			
	250	255	260
gaa ggc ctg ggc ggc gtc gac atg gct gct gaa aag ggc atc atg gat			931
Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu Lys Gly Ile Met Asp			
	265	270	275
ctg gca cca gcc aac gcg gaa gca ctt gcc gaa cta aat cca gac gtc			979
Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu Leu Asn Pro Asp Val			
	280	285	290
ttc gtg atg atg tcg gaa gga cta gtc tcg aca gga ggt atc gac ggt			
1027			
Phe Val Met Met Ser Glu Gly Leu Val Ser Thr Gly Gly Ile Asp Gly			

340 345 350

Pro Glu Gln Asn Thr Glu
355

<210> 837
<211> 645
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(622)
<223> RXA02136

<400> 837
tggttttgggt ctgggttact acgcgtattc ccgcaccatt cagcctcgta agtggcgctac 60

ccctcgtgca cgcgttgaaa ttggtgctga agtctagcgc atg cgc acg tta gtt 115
Met Arg Thr Leu Val
1 5

ctt ggc ggg gcc agg tct ggt aag tct gct ttt gca gaa tca ctt gtt 163
Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe Ala Glu Ser Leu Val
10 15 20

gga tct ggt ccc gtt ttg tat gtc gca acg gca agg cct tcg gga gat 211
Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala Arg Pro Ser Gly Asp
25 30 35

gat cct gaa ttc gcc gag cgc att gcg gtt cat gcg gag cgg cgc cca 259
Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His Ala Glu Arg Arg Pro
40 45 50

acg tct tgg gtg ttg gac gag gag ggg gac gtc gat aag ctt ctt gcc 307
Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val Asp Lys Leu Leu Ala
55 60 65

tcg cca ccg gcc atg ccg gtg ctc gtt gat gac ctg ggc acc tgg ctc 355
Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp Leu Gly Thr Trp Leu
70 75 80 85

acg cac gcc acc gat gcg tgc gac ggt tgg gag gcg agt tcg gcg cag 403
Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu Ala Ser Ser Ala Gln
90 95 100

ctt gag gcc aag atg gat ttg ctt atc gac gcc atc ctc cac ttt cag 451
Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala Ile Leu His Phe Gln
105 110 115

ggc gaa gat ctg gta att gtt tca cct gaa gtt ggt atg gga atc gtc 499
Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val Gly Met Gly Ile Val
120 125 130

ccg gaa tat aaa tct ggg cgc ctt ttt cgt gat cgc atc ggc aca ctt 547
Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp Arg Ile Gly Thr Leu
135 140 145

aat cag cgt gtc gca gcg att tgc gag agg gtt gtc ttc gtg gtt gct 595
Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val Val Phe Val Val Ala

150	155	160	165	
ggt ctg cca cta gag ttg aaa acg ttt taagaaaaca gtcggtttga				642
Gly Leu Pro Leu	Glu Leu Lys Thr Phe			
	170			

agg 645

```
<210> 838
<211> 174
<212> PRT
<213> Corynebacterium glutamicum
```

```
<400> 838
Met Arg Thr Leu Val Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe
  1             5              10             15
```

Ala Glu Ser Leu Val Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala
20 25 30

Arg Pro Ser Gly Asp Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His
35 40 45

Ala Glu Arg Arg Pro Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val
50 55 60

Asp Lys Leu Leu Ala Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp
65 70 75 80

Leu Gly Thr Trp Leu Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu
85 90 95

Ala Ser Ser Ala Gln Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala
100 105 110

Ile Leu His Phe Gln Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val
115 120 125

Gly Met Gly Ile Val Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp
130 135 140

Arg Ile Gly Thr Leu Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val
145 150 155 160

Val Phe Val Val Ala Gly Leu Pro Leu Glu Leu Lys Thr Phe
165 170

```
<210> 839
<211> 575
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (1)..(552)  
<223> RXN03114
```

<400> 839
act ccg ggg cat ttt gtt gcg ctc gcg cgg gag att gcg ggc gcg gtg 48

Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val
 1 5 10 15
 cgc cgc gag ttg acg gtg ggg ttg gat gct ggt gac ggt ccg att tta 96
 Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu
 20 25 30
 agg cag agc ttt gat gtt ggt ttt ttg ctt gtc gac gcc tcc ttc cac 144
 Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His
 35 40 45
 att cat atc aat ggc gtg tct act ggg cag tcg gtt gcg ccg gat gat 192
 Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp
 50 55 60
 gta gtt gag gtg gtg cgt ggt ttg gct gat gct tcg gag ttg tcc gtg 240
 Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val
 65 70 75 80
 gaa agt gtt gct gag ttg tgt act ccc gtg gca ccg gtt tca tta tct 288
 Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser
 85 90 95
 gag gca cag ggg aat cct gcg cct att ggg tgg ttg gag cat gat ggc 336
 Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly
 100 105 110
 gtg gtg tcg ttg ggt gcg ggt att cca ggg ggg cgg gtg gag gct cgt 384
 Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg
 115 120 125
 tta gcg cgt ttt att gcg gtg att gag gcg gag acc act att acc cca 432
 Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro
 130 135 140
 tgg aat tcg ttg atc att cat gat ttg tat gag ggt gtt gca gaa cag 480
 Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln
 145 150 155 160
 gtg gtg aag gtt ctg gct ccc atg ggg ttg gtt ttt gat gct aat tca 528
 Val Val Lys Val Leu Ala Pro Met Gly Leu Val Phe Asp Ala Asn Ser
 165 170 175
 ccg ctt ctg gag tca ccg gct ttg taactcgcca ttggtgcacg tct 575
 Pro Leu Leu Glu Ser Pro Ala Leu
 180

<210> 840

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 840

Thr Pro Gly His Phe Val Ala Leu Ala Arg Glu Ile Ala Gly Ala Val
 1 5 10 15
 Arg Arg Glu Leu Thr Val Gly Leu Asp Ala Gly Asp Gly Pro Ile Leu
 20 25 30
 Arg Gln Ser Phe Asp Val Gly Phe Leu Leu Val Asp Ala Ser Phe His

[illegible]

```
<210> 841
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1177)
<223> RXN01810
```

<400> 841
ccaccaccac aatgttgctc atcctcgcgg cgttcgttgt cgcaggtggc tccatgactc 60

gcttcaccgt cggcaaccg actggaaaat aaggcttcac atg aat aac gct ttt 115
Met Asn Asn Ala Phe
1 5

cga cgc acc ctt aca tcc gta gtc ctc gcc gct agc ttg gcc tta acg 163
Arg Arg Thr Leu Thr Ser Val Val Leu Ala Ala Ser Leu Ala Leu Thr
10 15 20

gcc tgc gca agc tgg gat tca cct acg gca tct tcc aat ggt gat ctg 211
Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser Ser Asn Gly Asp Leu
25 30 35

att gag gag atc cag gca agc tcc acc tca aca gat ccg cgc acc ttc 259
Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr Asp Pro Arg Thr Phe
40 45 50

aca ggc ttg agc atc gtg gaa gat atc ggc gat gtg gtt ccc gta acc 307
Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp Val Val Pro Val Thr

55	60	65	
gac aac gcc tca cca gct ctg cca gtt tct ttg acc gac gct gat ggc Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu Thr Asp Ala Asp Gly 70 75 80 85			355
aac gac gtg gtg gtg gag aac gtg tcc cgc atc ctc cca ctg gat ctc Asn Asp Val Val Val Glu Asn Val Ser Arg Ile Leu Pro Leu Asp Leu 90 95 100			403
tac gga acc tat tcc aaa acc atc gct ggc ctg gga ctc gtg gac aat Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu Gly Leu Val Asp Asn 105 110 115			451
att gtg ggt cgt act gtt agt tcc acc gag cct gca ttg gcg gac att Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro Ala Leu Ala Asp Ile 120 125 130			499
gag gtg gtc acc act ggc gga cac acc ctc aat gct gaa gcg atc ctt Glu Val Val Thr Thr Gly Gly His Thr Leu Asn Ala Glu Ala Ile Leu 135 140 145			547
aat tta cat ccg act ttg gtg atc atc gac cac tcg atc ggc cca cgc Asn Leu His Pro Thr Leu Val Ile Ile Asp His Ser Ile Gly Pro Arg 150 155 160 165			595
gaa gtc atc gat cag atc cgc gca gct ggt gtc gcc acg gtg atc atg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val Ala Thr Val Ile Met 170 175 180			643
tcg ccg cag cgt tcc att gcc tca att ggc gac gac atc cgc gac atc Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp Asp Ile Arg Asp Ile 185 190 195			691
gcc tcc gtc gtt gga ctt cct gaa gaa ggg gag aag ctc gcg gaa cgt Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu Lys Leu Ala Glu Arg 200 205 210			739
tcc gtt gct gaa gtc gaa gag gcc agc acg gtt gtc gat gaa ctc acc Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val Val Asp Glu Leu Thr 215 220 225			787
cca gaa gat ccc ctc aaa atg gta ttc ctc tat gcc cgc gga act ggt Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr Ala Arg Gly Thr Gly 230 235 240 245			835
gga gtg ttc ttc att ttg ggc gat gcc tat ggt gga cgc gat ctc att Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly Gly Arg Asp Leu Ile 250 255 260			883
gaa ggc ctg ggc ggc gtc gac atg gct gct gaa aag ggc atc atg gat Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu Lys Gly Ile Met Asp 265 270 275			931
ctg gca cca gcc aac gcg gaa gca ctt gcc gaa cta aat cca gac gtc Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu Leu Asn Pro Asp Val 280 285 290			979
ttc gtg atg atg tcg gaa gga cta gtc tcg aca gga ggt atc gac ggt 1027 Phe Val Met Met Ser Glu Gly Leu Val Ser Thr Gly Gly Ile Asp Gly			

295 300 305
 ctt atg gaa cgc ccc ggc att gct cag aca acc gcc gga caa aac caa
 1075
 Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr Ala Gly Gln Asn Gln
 310 315 320 325
 cga gta ctg gcg ctt ccc gat ggt caa tca ttg gcc ttt ggt gcc caa
 1123
 Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu Ala Phe Gly Ala Gln
 330 335 340
 act ggc gag ttg ttg ctc cgc gca tcc cgc gaa ctg tat gtg cag ggc
 1171
 Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu Leu Tyr Val Gln Gly
 345 350 355
 ggc gag tagatgggtg tgaaggaggt tga
 1200
 Gly Glu

<210> 842
 <211> 359
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 842
 Met Asn Asn Ala Phe Arg Arg Thr Leu Thr Ser Val Val Leu Ala Ala
 1 5 10 15
 Ser Leu Ala Leu Thr Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser
 20 25 30
 Ser Asn Gly Asp Leu Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr
 35 40 45
 Asp Pro Arg Thr Phe Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp
 50 55 60
 Val Val Pro Val Thr Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu
 65 70 75 80
 Thr Asp Ala Asp Gly Asn Asp Val Val Val Glu Asn Val Ser Arg Ile
 85 90 95
 Leu Pro Leu Asp Leu Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu
 100 105 110
 Gly Leu Val Asp Asn Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro
 115 120 125
 Ala Leu Ala Asp Ile Glu Val Val Thr Thr Gly Gly His Thr Leu Asn
 130 135 140
 Ala Glu Ala Ile Leu Asn Leu His Pro Thr Leu Val Ile Ile Asp His
 145 150 155 160
 Ser Ile Gly Pro Arg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val
 165 170 175

Ala Thr Val Ile Met Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp
 180 185 190

Asp Ile Arg Asp Ile Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu
 195 200 205

Lys Leu Ala Glu Arg Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val
 210 215 220

Val Asp Glu Leu Thr Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr
 225 230 235 240

Ala Arg Gly Thr Gly Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly
 245 250 255

Gly Arg Asp Leu Ile Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu
 260 265 270

Lys Gly Ile Met Asp Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu
 275 280 285

Leu Asn Pro Asp Val Phe Val Met Met Ser Glu Gly Leu Val Ser Thr
 290 295 300

Gly Gly Ile Asp Gly Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr
 305 310 315 320

Ala Gly Gln Asn Gln Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu
 325 330 335

Ala Phe Gly Ala Gln Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu
 340 345 350

Leu Tyr Val Gln Gly Gly Glu
 355

<210> 843
 <211> 963
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1) .. (933)
 <223> RXS03205

<400> 843
 gat tcc ggc att ccc acg cag ttg gtg gag ggc agc tgg ttt gaa ccg 48
 Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	
gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa	480
Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu	
145 150 155 160	
gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag	528
Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln	
165 170 175	
tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc	576
Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg	
180 185 190	
acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc	624
Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg	
195 200 205	
ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat	672
Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp	
210 215 220	
gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc	720
Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg	
225 230 235 240	
acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc	768
Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser	
245 250 255	
atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg	816
Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu	
260 265 270	
gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac	864
Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn	
275 280 285	
ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg	912

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300

ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aagccgtttt 963
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 844

<211> 311

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 844

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80

Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95

Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110

Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125

Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140

Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160

Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175

Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190

Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205

Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220

Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240

Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255

Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270

Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300

Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 845

<211> 956

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(933)

<223> FRXA00306

<400> 845

gat tcc ggc att ccc acg cag ttg gtg gag ggc agc tgg ttt gaa ccg	48
Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro	
1 5 10 15	
ggt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg	96
Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val	
20 25 30	
gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat	144
Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp	
35 40 45	
cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc	192
Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu	
50 55 60	
aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg	240
Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala	
65 70 75 80	
gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt	288
Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly	
85 90 95	
tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat	336
Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr	
100 105 110	
gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag	384
Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu	
115 120 125	
gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag	432
Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys	
130 135 140	

gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa 480
 Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160
 gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag 528
 Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175
 tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc 576
 Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190
 acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc 624
 Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205
 ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat 672
 Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220
 gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc 720
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240
 acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc 768
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255
 atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg 816
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270
 gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285
 ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300
 ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag 956
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 846

<211> 311

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 846

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
 1 5 10 15

Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu

50	55	60
Asn Pro Gly Gly Thr	Ala His Leu Leu Gly	Ala Trp Val His Ser Ala
65	70	75 80
Asp Gln Ser Trp Gln	Gln Arg Val Ala Glu Trp	Leu Pro Asp Asn Gly
	85	90 95
Tyr Val Ala Trp Val	Ile Glu Arg Asp Ala Val	Ser Pro Ala Gln Tyr
	100	105 110
Val Gly Thr Trp Leu	Ser Asp Glu Ser Leu Asp	Leu Arg Ser Pro Glu
	115	120 125
Ala Ala Ala Arg Thr	Thr Ala Trp Leu Asn His	Phe Glu Lys Ala Lys
	130	135 140
Val Gln Gly Val Gly	Phe Gly Phe Ile Ala Ile	Gln Arg Leu Glu Glu
	145	150 155 160
Asp Glu Ala Asp Glu	Lys Ser Asp Ile Leu Ala	Glu Ser Met Thr Gln
	165	170 175
Tyr Phe Glu Asp Pro	Leu Gly Pro Glu Ile Glu	Glu Tyr Phe Thr Arg
	180	185 190
Thr Ala Trp Leu Arg	Glu Gln Thr Arg Asp Ser	Ile Leu Ser Ser Arg
	195	200 205
Phe Lys Val Arg Pro	Gly Val Ala Arg Glu Gln	Ile Ser Leu Ala Asp
	210	215 220
Ala Glu Glu Gly Met	Gly Phe Ser Pro Val Thr	Leu Arg Leu Thr Arg
	225	230 235 240
Thr Asp Gly Pro Arg	Trp Ser His Asp Val Asp	Glu His Val Ala Ser
	245	250 255
Ile Val Ala Gly Leu	Asn Pro His Gly Leu Pro	Phe Glu Glu Ile Leu
	260	265 270
Glu Met Tyr Ala Met	Ala Gln Gly Ile Glu Gly	Glu Ser Leu His Asn
	275	280 285
Gly Ala Ile Ala Ala	Leu Val Asp Leu Ile Arg	His Gly Leu Val Leu
	290	295 300
Pro Ala Asp Leu Leu	Asp Ser	
	305	310

<210> 847

<211> 819

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(796)

<223> RXC01715

<400> 847

acatgttggtt ggaacatgcc ggcagagccg acactacgat tcattcgcta aagggctctgg 60
 ccactgacac tggcaaagat ccacgaaagg aagttaccct gtg agc gag ctc gat 115
 Val Ser Glu Leu Asp
 1 5
 att aaa cag ctc aac aaa ctg cag cgc tac tct cag tgg gcg gtg ttc 163
 Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser Gln Trp Ala Val Phe
 10 15 20
 cgt gct att cct gga gcg ctc gat gat gat cgc aca gaa gtc act gac 211
 Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg Thr Glu Val Thr Asp
 25 30 35
 caa gca gcc aag ttc ttt gcc gac ctt gaa gca gaa ggc aaa gtc act 259
 Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala Glu Gly Lys Val Thr
 40 45 50
 gtc cgt ggc att tac aac gcc tcc ggc ctg cgc gca gac gct gac tac 307
 Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg Ala Asp Ala Asp Tyr
 55 60 65
 atg atc tgg tgg cac gca gaa gaa ttc gaa gac att cag aag gcc ttc 355
 Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp Ile Gln Lys Ala Phe
 70 75 80 85
 gct gat ttc cgc cgc acc acc att ttg ggt cag gtt tct gag gtc ttc 403
 Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln Val Ser Glu Val Phe
 90 95 100
 tgg atc gga aac gct ctc cac cgt cca tct gag ttc aac aag gct cac 451
 Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu Phe Asn Lys Ala His
 105 110 115
 ttg cct tca ttc atc atg ggt gaa gaa gca aag gac tgg atc act gtt 499
 Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys Asp Trp Ile Thr Val
 120 125 130
 tac ccg ttc gtg cgc agc tac gac tgg tac atc atg gag ccc ttg aag 547
 Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile Met Glu Pro Leu Lys
 135 140 145
 cgt tcc cgc att ctc cgc gag cac gga caa gct gct gtg gaa ttc cca 595
 Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala Ala Val Glu Phe Pro
 150 155 160 165
 gat gtt cgt gcc aac act gtg ccg gct ttc gca ctg ggt gac tac gaa 643
 Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala Leu Gly Asp Tyr Glu
 170 175 180
 tgg gtg ctg gct ttc gag gct gat gag ttg cac cgc att gtc gat ttg 691
 Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His Arg Ile Val Asp Leu
 185 190 195
 atg cac aag atg cgt tac acc gag gct cgc ctc cac gtc cgt gag gag 739
 Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu His Val Arg Glu Glu
 200 205 210
 ctg cca ttt att tct gga cag cgc gtc gac att gca gat ctg att aag 787
 Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile Ala Asp Leu Ile Lys

215 220 225 819

gtt ctt cct taaaagctgc ttttctaaac gat
Val Leu Pro
230

<210> 848
<211> 232
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 848
Val Ser Glu Leu Asp Ile Lys Gln Leu Asn Lys Leu Gln Arg Tyr Ser
1 5 10 15
Gln Trp Ala Val Phe Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg
20 25 30
Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala
35 40 45
Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg
50 55 60
Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp
65 70 75 80
Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln
85 90 95
Val Ser Glu Val Phe Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu
100 105 110
Phe Asn Lys Ala His Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys
115 120 125
Asp Trp Ile Thr Val Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile
130 135 140
Met Glu Pro Leu Lys Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala
145 150 155 160
Ala Val Glu Phe Pro Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala
165 170 175
Leu Gly Asp Tyr Glu Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His
180 185 190
Arg Ile Val Asp Leu Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu
195 200 205
His Val Arg Glu Glu Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile
210 215 220
Ala Asp Leu Ile Lys Val Leu Pro
225 230

<210> 849
<211> 1587

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (1564)

<223> RXN00420

<400> 849

```

attcgtgaac tcattgatct ttaggcaata aatgtgagat tggacgattt cacgcttgct 60
ttcaccacct gaaaattttc gggggtaacc tttaaaggcg atg aac agt tct cac 115
Met Asn Ser Ser His
1 5

ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc 163
Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro
10 15 20

cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc 211
Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr
25 30 35

gct gag gta ctt acc acc cca gac cta gac atc att gtg gat gca gtc 259
Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val
40 45 50

cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc 307
Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg
55 60 65

ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa 355
Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln
70 75 80 85

aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac 403
Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His
90 95 100

tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc 451
Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr
105 110 115

ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct 499
Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro
120 125 130

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro
135 140 145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595
Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His
150 155 160 165

gtg gtc tcc atg gaa ctc ctc gtt gca gac gga cgc atc ctg cac ctc 643
Val Val Ser Met Glu Leu Leu Val Ala Asp Gly Arg Ile Leu His Leu
170 175 180

gag cca gaa ggc acc gcc gaa gac cca cag ggc gac ctg ttc tgg gca 691
Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly Asp Leu Phe Trp Ala

```

185										190										195										
acc gtt ggt ggc atg ggc ctg acc ggc atc atc gtc cgt gca cgc atc	Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile Val Arg Ala Arg Ile	739																												
200	205	210																												
cgc atg acc aag acg gaa acc gcc tac ttc att gcg gac acc gac cgc	Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile Ala Asp Thr Asp Arg	787																												
215	220	225																												
acc aac aac ttg gaa gaa acc gtt gcg ttc cac tcc gac gga tca gag	Thr Asn Asn Leu Glu Thr Val Ala Phe His Ser Asp Gly Ser Glu	835																												
230	235	240	245																											
cac aac tac acc tat tct tct gcg tgg ttc gat gtc atc agc cct gag	His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp Val Ile Ser Pro Glu	883																												
250	255	260																												
cca aag ctt ggc cgc tcc acc atc tcc cgt ggt tcc ctg gca aca ctt	Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly Ser Leu Ala Thr Leu	931																												
265	270	275																												
gct cag ctg gaa gaa ttg gca cca aag ctg gcc aag gat cca ctg aag	Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala Lys Asp Pro Leu Lys	979																												
280	285	290																												
ttt aat gct cca cag ctg atg aag gtt cca gat atc ttc cca tcc tgg	Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp Ile Phe Pro Ser Trp																													
1027	300	305																												
act ttg aac aag ctg acc ctt tcc gca gtc ggt gtg gct tac tac gcc	Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr Ala																													
1075	315	320	325																											
atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc tac	Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe Tyr																													
1123	330	335	340																											
caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc aag	Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser Lys																													
1171	345	350	355																											
ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag cct	Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu Pro																													
1219	360	365	370																											
ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc gca	Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser Ala																													
1267	375	380	385																											
ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg tcc	Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu Ser																													
1315	390	395	400																											
			405																											

tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc cca
1363

Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg Pro
410 415 420

ggc ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa ttc
1411

Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu Phe
425 430 435

ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag aac
1459

Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu Asn
440 445 450

ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga aat
1507

Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg Asn
455 460 465

gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga ctt
1555

Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg Leu
470 475 480 485

gag ctt tct taagaaaggg cttgaactaa aca
1587

Glu Leu Ser

<210> 850

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 850

Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala
1 5 10 15

His Gly Ala Leu Pro Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg
20 25 30

Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile
35 40 45

Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro
50 55 60

Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr
65 70 75 80

Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro
85 90 95

Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val
100 105 110

Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr
115 120 125

Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly
 130 135 140
 Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly
 145 150 155 160
 Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala Asp Gly
 165 170 175
 Arg Ile Leu His Leu Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly
 180 185 190
 Asp Leu Phe Trp Ala Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile
 195 200 205
 Val Arg Ala Arg Ile Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile
 210 215 220
 Ala Asp Thr Asp Arg Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His
 225 230 235 240
 Ser Asp Gly Ser Glu His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp
 245 250 255
 Val Ile Ser Pro Glu Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly
 260 265 270
 Ser Leu Ala Thr Leu Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala
 275 280 285
 Lys Asp Pro Leu Lys Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp
 290 295 300
 Ile Phe Pro Ser Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly
 305 310 315 320
 Val Ala Tyr Tyr Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn
 325 330 335
 Leu Thr Gln Phe Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg
 340 345 350
 Gly Tyr Gly Ser Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr
 355 360 365
 Glu Ala Val Glu Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser
 370 375 380
 Gly His Tyr Ser Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn
 385 390 395 400
 Arg Ala Pro Leu Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp
 405 410 415
 Phe Pro Ile Arg Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys
 420 425 430
 Arg Val Met Glu Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg
 435 440 445
 Thr Ser Ala Glu Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp


```

      450              455              460
Leu Lys Thr Arg Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp
465              470              475              480

Met Ser Arg Arg Leu Glu Leu Ser
      485

<210> 851
<211> 563
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(540)
<223> FRXA00420

<400> 851
tgg act ttg aac aag ctg acc ctt tcc gca gtc ggt gtg gct tac tac   48
Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr
   1              5              10              15

gcc atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc   96
Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe
      20              25              30

tac caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc   144
Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser
      35              40              45

aag ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag   192
Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu
      50              55              60

cct ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc   240
Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser
      65              70              75              80

gca ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg   288
Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu
      85              90              95

tcc tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc   336
Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg
      100             105             110

cca ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa   384
Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu
      115             120             125

ttc ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag   432
Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu
      130             135             140

aac ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga   480
Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg
      145             150             155             160

aat gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga   528

```

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg
 165 170 175

ctt gag ctt tct taagaaaggg cttgaactaa aca
 Leu Glu Leu Ser
 180

563

<210> 852

<211> 180

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 852

Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly Val Ala Tyr Tyr
 1 5 10 15

Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe
 20 25 30

Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser
 35 40 45

Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu
 50 55 60

Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser
 65 70 75 80

Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu
 85 90 95

Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg
 100 105 110

Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu
 115 120 125

Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu
 130 135 140

Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg
 145 150 155 160

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg
 165 170 175

Leu Glu Leu Ser
 180

<210> 853

<211> 622

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(622)

<223> FRXA00426

<400> 853

```

attcgtgaac tcatggatct ttaggcaata aatgtgagat tggacgattt cacgcttgtc 60
ttcaccacct gaaaattttc gggggtaacc tttaaaggcg atg aac agt tct cac 115
                                         Met Asn Ser Ser His
                                         1 5

ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc 163
Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro
                        10 15 20

cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc 211
Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr
                        25 30 35

gct gag gta ctt acc acc cca gac cta gac atc att gtg gat gca gtc 259
Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val
                        40 45 50

cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc 307
Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg
                        55 60 65

ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa 355
Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln
                        70 75 80 85

aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac 403
Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His
                        90 95 100

tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc 451
Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr
                        105 110 115

ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct 499
Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro
                        120 125 130

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547
Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro
                        135 140 145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595
Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His
                        150 155 160 165

gtg gtc tcc atg gaa ctc ctc gtt gca 622
Val Val Ser Met Glu Leu Leu Val Ala
                        170

```

<210> 854

<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 854

```

Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala
1 5 10 15

```

```
<210> 855
<211> 930
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(907)  
<223> RXN00708
```

```

<400> 855
cctgcgtatc ggctgccttt ttgaattcctt ttcctcctcg aggcctaacc ttcaattcct 60

taccgatccc cttccctgaa gtttcgctaa cctggcgtac atg act ctt tcc ctt 115
Met Thr Leu Ser Leu
1 5

cct cca att ggt ttc ggc acc gtt cat ctt gat ggc gca cct ggc gtt 163
Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp Gly Ala Pro Gly Val
10 15 20

gaa gcc atc gct act gcc att gat gct ggt tac cgc ctc atc gac acc 211
Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr Arg Leu Ile Asp Thr
25 30 35

gcg tac aac tat gaa aat gaa ggt acc gtg ggc aag gct gtc cgc gag 259
Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly Lys Ala Val Arg Glu
40 45 50

tcg ggt gtc ccc cgc gag gaa ttg att gtt acc agt aag ctc cct gcc 307

```

Ser	Gly	Val	Pro	Arg	Glu	Glu	Leu	Ile	Val	Thr	Ser	Lys	Leu	Pro	Gly		
55						60					65						
cgc	ttc	cat	gct	cgc	gat	cta	gga	cgc	gtc	cgc	att	gag	gaa	agt	cta	355	
Arg	Phe	His	Ala	Arg	Asp	Leu	Gly	Arg	Val	Arg	Ile	Glu	Glu	Ser	Leu	85	
70					75				80								
tac	cgc	ctc	aac	tta	gat	tac	atc	gat	ctc	ctc	ttg	att	cac	tgg	cct	403	
Tyr	Arg	Leu	Asn	Leu	Asp	Tyr	Ile	Asp	Leu	Leu	Leu	Ile	His	Trp	Pro	100	
				90					95								
aat	ccc	agc	aag	gat	ctc	tac	gtc	gag	gcg	tgg	gaa	acg	ctg	att	gaa	451	
Asn	Pro	Ser	Lys	Asp	Leu	Tyr	Val	Glu	Ala	Trp	Glu	Thr	Leu	Ile	Glu	115	
			105					110									
gtc	cgc	gat	gct	ggc	ctg	gtc	aag	cac	atc	gga	gtg	tct	aac	ttc	ctt	499	
Val	Arg	Asp	Ala	Gly	Leu	Val	Lys	His	Ile	Gly	Val	Ser	Asn	Phe	Leu	130	
			120				125										
cca	aat	cac	att	gat	cgc	ctg	cgc	cgc	gaa	acc	ggt	gaa	ctg	ccg	gcc	547	
Pro	Asn	His	Ile	Asp	Arg	Leu	Arg	Arg	Glu	Thr	Gly	Glu	Leu	Pro	Ala	145	
	135					140											
gtt	aac	cag	atc	gag	ttg	cac	ccc	tat	ttc	ccg	cag	gtg	gag	cag	gta	595	
Val	Asn	Gln	Ile	Glu	Leu	His	Pro	Tyr	Phe	Pro	Gln	Val	Glu	Gln	Val	165	
	150				155					160							
gat	ttc	cac	gat	gag	ctg	ggc	atc	att	acc	gag	gcc	tgg	agc	ccg	ctc	643	
Asp	Phe	His	Asp	Glu	Leu	Gly	Ile	Ile	Thr	Glu	Ala	Trp	Ser	Pro	Leu	180	
				170					175								
agc	aac	ggt	cgc	gga	ctc	gtc	gaa	gag	cca	ttg	ctc	aag	gaa	atc	ggc	691	
Ser	Asn	Gly	Arg	Gly	Leu	Val	Glu	Glu	Pro	Leu	Leu	Lys	Glu	Ile	Gly	195	
			185					190									
gag	cgc	tac	ggg	gtc	ggc	agc	ggc	gaa	atc	gcc	ctc	gct	tgg	cat	cac	739	
Glu	Arg	Tyr	Gly	Val	Gly	Ser	Gly	Glu	Ile	Ala	Leu	Ala	Trp	His	His	210	
		200					205										
gcc	agg	gga	atc	gtt	ccg	att	cca	cgc	tcc	acc	aac	ccg	gcc	agg	cag	787	
Ala	Arg	Gly	Ile	Val	Pro	Ile	Pro	Arg	Ser	Thr	Asn	Pro	Ala	Arg	Gln	225	
		215				220											
cgc	agc	aac	ttg	gag	gcg	gta	aag	att	tcg	ctt	atc	gac	gaa	gac	gtc	835	
Arg	Ser	Asn	Leu	Glu	Ala	Val	Lys	Ile	Ser	Leu	Ile	Asp	Glu	Asp	Val	245	
					235					240							
cag	gcg	att	acc	gct	ttg	gcg	cgc	aaa	aac	ggc	cgg	atc	aaa	gat	caa	883	
Gln	Ala	Ile	Thr	Ala	Leu	Ala	Arg	Lys	Asn	Gly	Arg	Ile	Lys	Asp	Gln	260	
				250					255								
gat	cca	gcc	gtc	tat	gaa	gaa	ttc	tagatagtta	catcaagggtt	ccg						930	
Asp	Pro	Ala	Val	Tyr	Glu	Glu	Phe									265	

<210> 856

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 856

```

Met Thr Leu Ser Leu Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp
 1           5           10           15

Gly Ala Pro Gly Val Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr
          20           25           30

Arg Leu Ile Asp Thr Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly
          35           40           45

Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu Ile Val Thr
          50           55           60

Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly Arg Val Arg
          65           70           75           80

Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile Asp Leu Leu
          85           90           95

Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val Glu Ala Trp
          100          105          110

Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys His Ile Gly
          115          120          125

Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg Arg Glu Thr
          130          135          140

Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro Tyr Phe Pro
          145          150          155          160

Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile Ile Thr Glu
          165          170          175

Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu Glu Pro Leu
          180          185          190

Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly Glu Ile Ala
          195          200          205

Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro Arg Ser Thr
          210          215          220

Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys Ile Ser Leu
          225          230          235          240

Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg Lys Asn Gly
          245          250          255

Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
          260          265

```

<210> 857

<211> 695

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1) .. (672)

<223> FRXA00708

<400> 857

acc gtg ggc aag gct gtc cgc gag tcg ggt gtc ccc cgc gag gaa ttg	48
Thr Val Gly Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu	
1 5 10 15	
att gtt acc agt aag ctc cct ggc cgc ttc cat gct cgc gat cta gga	96
Ile Val Thr Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly	
20 25 30	
cgc gtc cgc att gag gaa agt cta tac cgc ctc aac tta gat tac atc	144
Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile	
35 40 45	
gat ctc ctc ttg att cac tgg cct aat ccc agc aag gat ctc tac gtc	192
Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val	
50 55 60	
gag gcg tgg gaa acg ctg att gaa gtc cgc gat gct ggc ctg gtc aag	240
Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys	
65 70 75 80	
cac atc gga gtg tct aac ttc ctt cca aat cac att gat cgc ctg cgc	288
His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg	
85 90 95	
cgc gaa acc ggt gaa ctg ccg gcc gtt aac cag atc gag ttg cac ccc	336
Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro	
100 105 110	
tat ttc ccg cag gtg gag cag gta gat ttc cac gat gag ctg ggc atc	384
Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile	
115 120 125	
att acc gag gcc tgg agc ccg ctc agc aac ggt cgc gga ctc gtc gaa	432
Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu	
130 135 140	
gag cca ttg ctc aag gaa atc ggc gag cgc tac ggg gtc ggc agc ggc	480
Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly	
145 150 155 160	
gaa atc gcc ctc gct tgg cat cac gcc agg gga atc gtt ccg att cca	528
Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro	
165 170 175	
cgc tcc acc aac ccg gcc agg cag cgc agc aac ttg gag gcg gta aag	576
Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys	
180 185 190	
att tcg ctt atc gac gaa gac gtc cag gcg att acc gct ttg gcg cgc	624
Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg	
195 200 205	
aaa aac ggc cgg atc aaa gat caa gat cca gcc gtc tat gaa gaa ttc	672
Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe	
210 215 220	
tagatagttta catcaagggtt ccg	695

<210> 858

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 858

Thr Val Gly Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu
 1 5 10 15

Ile Val Thr Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly
 20 25 30

Arg Val Arg Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile
 35 40 45

Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val
 50 55 60

Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys
 65 70 75 80

His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg
 85 90 95

Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro
 100 105 110

Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile
 115 120 125

Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu
 130 135 140

Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly
 145 150 155 160

Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro
 165 170 175

Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys
 180 185 190

Ile Ser Leu Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg
 195 200 205

Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
 210 215 220

<210> 859

<211> 1038

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1015)

<223> RXA02373

<400> 859

```

aaagtcataag ctcattgtaa ttcagtgtag ataggcgtac ggtgggctat ccaattcacc 60

tcaacctaag ggcgattttg gtgcgcatca aggagaaaat atg tct gtt gtg ggt 115
Met Ser Val Val Gly
1 5

acc ggc cta ttc ttt gga tcc ccg gag gaa gag cgg gat aag ttg atg 163
Thr Gly Leu Phe Phe Gly Ser Pro Glu Glu Glu Arg Asp Lys Leu Met
10 15 20

caa tct ttg atg gat cag aag aat aag ctt tcg aag tct gaa ggt atc 211
Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser Lys Ser Glu Gly Ile
25 30 35

cca ttg gtc acc ttg aat gat gga aaa acc att cct cag ctt ggt ttt 259
Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile Pro Gln Leu Gly Phe
40 45 50

ggt gtg ttc aag gta gat ccc gat gaa gca gag cgc gta gtt acc gaa 307
Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu Arg Val Val Thr Glu
55 60 65

gca ctt gag gta ggt tac cgc cac atc gat act gct gcg att tac ggc 355
Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr Ala Ala Ile Tyr Gly
70 75 80 85

aat gag gaa ggt gtc ggc cga gct att gct aag tcc ggc att cct cgt 403
Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys Ser Gly Ile Pro Arg
90 95 100

gaa gag ctg ttt att act acc aag ttg tgg aac gat cgc cac ctg gat 451
Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn Asp Arg His Leu Asp
105 110 115

gta gaa gct gct ttt gag gag tct ctg cag aag ctg ggc ttg gat tat 499
Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys Leu Gly Leu Asp Tyr
120 125 130

gta gat ctg tac ttg gtg cac tgg ccg gca ccg aag aac gat aat tat 547
Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro Lys Asn Asp Asn Tyr
135 140 145

gtt gct gca tgg aag ggc ttg gaa aag ctc ggt gac cgt gct cgt tcc 595
Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly Asp Arg Ala Arg Ser
150 155 160 165

atc ggt gtg tgc aac ttc ctg cca gag cac cta gaa aag ctg ctg gca 643
Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu Glu Lys Leu Leu Ala
170 175 180

gag gca acc act gtg cct gcc att aac cag att gag ctg cac cca gct 691
Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile Glu Leu His Pro Ala
185 190 195

ttg cag cag cgc gat gct gtt gag gca tct ctt gca gca ggc atc act 739
Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu Ala Ala Gly Ile Thr
200 205 210

```

gtg gag tcg tgg ggt cct ctg gga cag ggg cgt ttt gat ctt ggc gct 787
 Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg Phe Asp Leu Gly Ala
 215 220 225

gag gaa cca atc gca gct gca gcg aag aac cat gga aag acc cca gct 835
 Glu Glu Pro Ile Ala Ala Ala Ala Lys Asn His Gly Lys Thr Pro Ala
 230 235 240 245

cag gtt gtt atc cgt tgg cac ctg cag aac ggt ttc gtt gtg ttc ccc 883
 Gln Val Val Ile Arg Trp His Leu Gln Asn Gly Phe Val Val Phe Pro
 250 255 260

aag act gtg act aag agc cgc atg gtg gaa aac atc gac gtg ttt gat 931
 Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn Ile Asp Val Phe Asp
 265 270 275

ttc gaa ctc agt gat gag gag atg gct gcg atc act gct ctt gag cgc 979
 Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile Thr Ala Leu Glu Arg
 280 285 290

aat gat cgt ggt ggt tca cac ccg aat gat ctg aac tagaaataag
 1025
 Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu Asn
 295 300 305

gtaaggccct gca
 1038

<210> 860
 <211> 305
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 860
 Met Ser Val Val Gly Thr Gly Leu Phe Phe Gly Ser Pro Glu Glu Glu
 1 5 10 15

Arg Asp Lys Leu Met Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser
 20 25 30

Lys Ser Glu Gly Ile Pro Leu Val Thr Leu Asn Asp Gly Lys Thr Ile
 35 40 45

Pro Gln Leu Gly Phe Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu
 50 55 60

Arg Val Val Thr Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr
 65 70 75 80

Ala Ala Ile Tyr Gly Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys
 85 90 95

Ser Gly Ile Pro Arg Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn
 100 105 110

Asp Arg His Leu Asp Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys
 115 120 125

Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Val His Trp Pro Ala Pro
 130 135 140

Lys Asn Asp Asn Tyr Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly
 145 150 155 160
 Asp Arg Ala Arg Ser Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu
 165 170 175
 Glu Lys Leu Leu Ala Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile
 180 185 190
 Glu Leu His Pro Ala Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu
 195 200 205
 Ala Ala Gly Ile Thr Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg
 210 215 220
 Phe Asp Leu Gly Ala Glu Glu Pro Ile Ala Ala Ala Lys Asn His
 225 230 235 240
 Gly Lys Thr Pro Ala Gln Val Val Ile Arg Trp His Leu Gln Asn Gly
 245 250 255
 Phe Val Val Phe Pro Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn
 260 265 270
 Ile Asp Val Phe Asp Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile
 275 280 285
 Thr Ala Leu Glu Arg Asn Asp Arg Gly Gly Ser His Pro Asn Asp Leu
 290 295 300

Asn
 305

<210> 861
 <211> 1683
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1660)
 <223> RXS00389

<400> 861
 ccaccactgc gtaacctttc cgagcaagat atcgcgaggacc tgtcggattt gcttgccacc 60
 tctggcgcag gttcctaccg ccttcagttg aggtgaaagc atg atc acc gca acc 115
 Met Ile Thr Ala Thr
 1 5
 gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163
 Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
 10 15 20
 aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211
 Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
 25 30 35
 cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259

Pro	Ser	Tyr	Ser	Leu	Ala	Asn	Ser	Ala	Gln	Leu	Arg	Ala	Ala	Thr	Thr		
		40					45					50					
tcg	gcg	aag	cga	gct	ttt	gaa	agc	tac	cga	ctc	act	act	cca	gag	gtt	307	
Ser	Ala	Lys	Arg	Ala	Phe	Glu	Ser	Tyr	Arg	Leu	Thr	Thr	Pro	Glu	Val		
	55					60				65							
aga	gca	gat	ttc	ctg	gat	tcc	atc	gct	gac	aac	atc	gat	gcg	cta	tcc	355	
Arg	Ala	Asp	Phe	Leu	Asp	Ser	Ile	Ala	Asp	Asn	Ile	Asp	Ala	Leu	Ser		
70				75					80					85			
ggc	gag	atc	gtg	caa	cgg	gcg	agc	ctg	gag	aca	ggg	ttg	gga	act	acc	403	
Gly	Glu	Ile	Val	Gln	Arg	Ala	Ser	Leu	Glu	Thr	Gly	Leu	Gly	Thr	Thr		
			90					95					100				
cga	ctc	aca	ggc	gaa	gta	gcc	cgc	acc	agc	aac	cag	ctc	cgc	ctg	ttt	451	
Arg	Leu	Thr	Gly	Glu	Val	Ala	Arg	Thr	Ser	Asn	Gln	Leu	Arg	Leu	Phe		
			105					110				115					
gca	gaa	acc	gtg	aga	agc	gga	cag	ttc	cac	cga	gta	cgc	att	gaa	cga	499	
Ala	Glu	Thr	Val	Arg	Ser	Gly	Gln	Phe	His	Arg	Val	Arg	Ile	Glu	Arg		
		120					125					130					
gga	ccg	cgg	att	gat	ctt	cgc	cag	cgt	cag	gtt	ccg	ttg	gga	cca	gtc	547	
Gly	Pro	Arg	Ile	Asp	Leu	Arg	Gln	Arg	Gln	Val	Pro	Leu	Gly	Pro	Val		
	135					140					145						
gcg	gta	ttc	ggg	gca	agc	aac	ttc	ccc	gtc	gct	ttc	tct	act	gct	ggg	595	
Ala	Val	Phe	Gly	Ala	Ser	Asn	Phe	Pro	Val	Ala	Phe	Ser	Thr	Ala	Gly		
150					155				160						165		
ggc	gat	aca	gca	tca	gcg	ttg	gct	gca	ggc	tgc	cct	gtg	gtt	ttt	aag	643	
Gly	Asp	Thr	Ala	Ser	Ala	Leu	Ala	Ala	Gly	Cys	Pro	Val	Val	Phe	Lys		
			170					175						180			
gcg	cat	aat	gcg	cac	cct	gga	aca	gct	gag	ctc	gtc	ggg	caa	gcg	gtg	691	
Ala	His	Asn	Ala	His	Pro	Gly	Thr	Ala	Glu	Leu	Val	Gly	Gln	Ala	Val		
			185					190					195				
cgg	gga	gcc	gtc	gaa	aag	cat	gag	ttt	gat	gct	ggg	gtg	ttt	aac	ctt	739	
Arg	Gly	Ala	Val	Glu	Lys	His	Glu	Phe	Asp	Ala	Gly	Val	Phe	Asn	Leu		
		200					205					210					
gtc	tac	ggc	cgt	ggc	gtg	gaa	att	ggc	cag	gag	ctg	gct	gcg	gat	ccg	787	
Val	Tyr	Gly	Arg	Gly	Val	Glu	Ile	Gly	Gln	Glu	Leu	Ala	Ala	Asp	Pro		
	215					220					225						
aat	atc	acg	gca	atc	ggg	ttt	acc	ggg	tca	cgc	cag	ggg	ggg	ttg	gca	835	
Asn	Ile	Thr	Ala	Ile	Gly	Phe	Thr	Gly	Ser	Arg	Gln	Gly	Gly	Leu	Ala		
230					235					240				245			
ctg	tca	cag	act	gcg	ttt	agc	cgc	cca	gtt	ccc	gtt	cca	gtc	ttt	gca	883	
Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala		
				250				255						260			
gaa	atg	agt	gcc	acc	aac	cct	gtg	ttc	gtc	ttc	ccc	ggc	gcg	ctg	gcg	931	
Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala		
			265					270					275				
gat	ttg	gat	gca	tcg	agt	tcc	ttg	gct	gag	gcg	ttt	acc	gct	tcc	gtc	979	
Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val		

280	285	290
acc ggc agt tcc ggg caa ttg tgc acc aag cct ggc ctc gtt ttc atc 1027		
Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro Gly Leu Val Phe Ile 295 300 305		
ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa 1075		
Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys 310 315 320 325		
ttt aaa gaa acc acg ggt caa acg atg ctc acg caa ggc atc gct cag 1123		
Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln 330 335 340		
gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa 1171		
Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys 345 350 355		
atc ctc gcc caa ggc acc ccc gga gat gga gag aac gcg ccg ggc ccg 1219		
Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro 360 365 370		
gtg gtg ttt gaa agt gat gtg cag gcg ttg cta aat aat gtg gtg ttg 1267		
Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu 375 380 385		
cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc 1315		
Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser 390 395 400 405		
ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca 1363		
Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr 410 415 420		
gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcg aaa ctt 1411		
Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu 425 430 435		
atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg 1459		
Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp 440 445 450		
cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat 1507		
Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr 455 460 465		
ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc 1555		
Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile 470 475 480 485		

gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg
1603

Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu
490 495 500

ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa
1651

Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu
505 510 515

ata gac cgt taatagctgg tctttacatt tgc
1683

Ile Asp Arg
520

<210> 862

<211> 520

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 862

Met Ile Thr Ala Thr Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu
1 5 10 15

Trp Val Ala Gly Lys Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr
20 25 30

Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu
35 40 45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu
50 55 60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn
65 70 75 80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr
85 90 95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn
100 105 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg
115 120 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val
130 135 140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala
145 150 155 160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys
165 170 175

Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu
180 185 190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
195 200 205

Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
 210 215 220
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
 225 230 235 240
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
 245 250 255
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
 260 265 270
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
 275 280 285
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
 290 295 300
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala
 305 310 315 320
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr
 325 330 335
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala
 340 345 350
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu
 355 360 365
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu
 370 375 380
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val
 385 390 395 400
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu
 405 410 415
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln
 420 425 430
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val
 435 440 445
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile
 450 455 460
 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val
 465 470 475 480
 Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr
 485 490 495
 Phe Pro Ala Glu Leu Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp
 500 505 510
 Ala Val Pro Arg Glu Ile Asp Arg
 515 520

<210> 863

<211> 882

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (859)

<223> RXS00419

<400> 863

gctgggttgaa gactcgaaat gagatcgacc caaccggagt ctttgcattct gacatgtccc 60

gccgacttga gctttcttaa gaaagggctt gaactaaaca atg ctt aac gca gtg 115
Met Leu Asn Ala Val
1 5

ggc aaa gcc caa aac att ctc ctt ctt ggt gga acc tct gag atc ggt 163
Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly Thr Ser Glu Ile Gly
10 15 20

att tcc att gtc tcc cgc ttc ctc aag cag ggt cca tcc cat gtg acc 211
Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly Pro Ser His Val Thr
25 30 35

ttg	gca	gcg	cgt	aaa	gat	tcc	cca	cgc	gtg	gac	gca	gca	gtc	gca	gag	259
Leu	Ala	Ala	Arg	Lys	Asp	Ser	Pro	Arg	Val	Asp	Ala	Ala	Val	Ala	Glu	
		40					45					50				

atc aaa gca gct ggc gct gct tcc gtt gct gtt gtt gat ttc gat gcg 307
Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val Val Asp Phe Asp Ala
55 60 65

ctc gac acc gaa tcc cac cct gca gcc atc gac gca gcc ttt gaa aac 355
Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp Ala Ala Phe Glu Asn
70 75 80 85

ggc gac gtt gac gta gca atc gtg gct ttc ggc atc ctc ggc gac aac 403
Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly Ile Leu Gly Asp Asn
90 95 100

gaa gca cag tgg cgc gac caa gca cta gca gtg gaa gca acc acc gtg 451
Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val Glu Ala Thr Thr Val
105 110 115

aac tac acc gcc ggc gtt tcc gta ggt gta ctg ctg ggc cag aaa ttt 499
Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu Leu Gly Gln Lys Phe
120 125 130

gag cag cag ggc cac ggc acc atc gtg gca ttg tcc tct gtg gca ggc 547
Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu Ser Ser Val Ala Gly
135 140 145

cag cga gtc cgc cgc tcc aac ttt gtc tac ggc tcc gcc aag gca ggt 595
Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly Ser Ala Lys Ala Gly
150 155 160 165

ttc gac ggt ttc tac acc cag ctc ggc gaa gcc ctg cgt gga tcc ggt 643
Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly Ser Gly
170 175 180

gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag atg tcc 691
 Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys Met Ser
 185 190 195

gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac gtg gca 739
 Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp Val Ala
 200 205 210

gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc ttt gtc 787
 Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile Phe Val
 215 220 225

cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att ccg cga 835
 His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile Pro Arg
 230 235 240 245

gca atc ttc cgc aag ctg ccg ttc taacggaagt tacggaagtt acg 882
 Ala Ile Phe Arg Lys Leu Pro Phe
 250

<210> 864

<211> 253

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 864

Met Leu Asn Ala Val Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly
 1 5 10 15

Thr Ser Glu Ile Gly Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly
 20 25 30

Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp
 35 40 45

Ala Ala Val Ala Glu Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val
 50 55 60

Val Asp Phe Asp Ala Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp
 65 70 75 80

Ala Ala Phe Glu Asn Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly
 85 90 95

Ile Leu Gly Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val
 100 105 110

Glu Ala Thr Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu
 115 120 125

Leu Gly Gln Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu
 130 135 140

Ser Ser Val Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly
 145 150 155 160

Ser Ala Lys Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala
 165 170 175

Leu Arg Gly Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val
 180 185 190
 Arg Thr Lys Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn
 195 200 205
 Arg Glu Asp Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys
 210 215 220
 Asp Ile Ile Phe Val His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe
 225 230 235 240
 Gln Phe Ile Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe
 245 250

<210> 865
 <211> 1673
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1650)
 <223> RXC00416

<400> 865
 ctg gcg tct tac tta agc cca act gcg ctg gtg gtt gcg gtg ttg gct 48
 Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
 1 5 10 15
 att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac 96
 Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
 20 25 30
 cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc 144
 Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
 35 40 45
 ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga 192
 Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50 55 60
 tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt 240
 Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65 70 75 80
 tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct 288
 Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
 85 90 95
 tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg 336
 Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
 100 105 110
 gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat 384
 Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
 115 120 125
 tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg 432
 Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met

130	135	140	
ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala 145 150 155 160			480
ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe 165 170 175			528
acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala 180 185 190			576
gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu 195 200 205			624
ggt ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu 210 215 220			672
ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His 225 230 235 240			720
tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser 245 250 255			768
agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val 260 265 270			816
cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val 275 280 285			864
ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn 290 295 300			912
acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala 305 310 315 320			960
acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat 1008 Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr 325 330 335			
cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc 1056 Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr 340 345 350			
aat cta att gtg gtc ctc gtg ctg ctt ggc ggc ctc tac tac gcg caa 1104 Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln 355 360 365			

gat ctg ccg cag aag aac gca cga gct atc gat ctg gcc tat acc gat
 1152
 Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
 370 375 380

 act gat ggc tac ggc gag cgc gcg gat ctg tat ccg gcc gga gct gca
 1200
 Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
 385 390 395 400

 cgt tat tac aag gac atc aac gat cat ctg ctt gat caa gga ttc gag
 1248
 Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
 405 410 415

 cct tcc gaa act gtc gtg ctg aca gac gaa ctc gat ttc atg tcc tac
 1296
 Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
 420 425 430

 tac cct tat cgc gga tac caa gct ttt act tcc cac tac gcc aac ccg
 1344
 Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
 435 440 445

 ctt ggt gag ttc gga aac agg aac gca ttc atc gaa gat ctc gcg atc
 1392
 Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
 450 455 460

 cga agc tgg gat gag ttg gct gat cct caa caa ttc agc gac gcc ttg
 1440
 Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
 465 470 475 480

 aac acc tct cca tgg acg atc cct gag gtg ttc atc ttc cgt ggc tcc
 1488
 Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
 485 490 495

 atc gat gat cct gac gcc ggt tgg aaa tac gac gtg gct gaa gat ctg
 1536
 Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
 500 505 510

 tac ccg aac aat cca aac gtg cgc ttc cgc ggc gtg tac ttt aac ccg
 1584
 Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
 515 520 525

 gag tca ttt gat cag atg tgg cag acc aag caa gtg gga cct ttc gtg
 1632
 Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
 530 535 540

 gtg gta acg cac aat gag taattcctca ccaaacgacc caa
 1673
 Val Val Thr His Asn Glu
 545 550

<210> 866

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 866

Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
 1 5 10 15

Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
 20 25 30

Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
 35 40 45

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50 55 60

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65 70 75 80

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
 85 90 95

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
 100 105 110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
 115 120 125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
 130 135 140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
 145 150 155 160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
 165 170 175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
 180 185 190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
 195 200 205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
 210 215 220

Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
 225 230 235 240

Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
 245 250 255

Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
 260 265 270

Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
 275 280 285

Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn

290	295	300
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala 305 310 315 320		
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr 325 330 335		
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr 340 345 350		
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln 355 360 365		
Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp 370 375 380		
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala 385 390 395 400		
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu 405 410 415		
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr 420 425 430		
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro 435 440 445		
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile 450 455 460		
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu 465 470 475 480		
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser 485 490 495		
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu 500 505 510		
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro 515 520 525		
Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val 530 535 540		
Val Val Thr His Asn Glu 545 550		

<210> 867

<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> RXC02206

<400> 867

```

ggcaggatct gctgctgcgg ctaggagggt tatctcttca ttcacccgat ctaccgtact 60

accttatgac ctca gtagtg tgggtgggcgt gaaacagcga atg gtc ggt tca agt 115
Met Val Gly Ser Ser
1 5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
10 15 20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
25 30 35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
40 45 50

gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
55 60 65

gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc 355
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
70 75 80 85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat 403
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp
90 95 100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
105 110 115

ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg 499
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu
120 125 130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga 547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly
135 140 145

tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca 595
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala
150 155 160 165

gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg 643
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu
170 175 180

ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta 691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu
185 190 195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act 739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr
200 205 210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca 787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr

```

215 220 225
 gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc 835
 Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile
 230 235 240 245
 att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc 883
 Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro
 250 255 260
 gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct 931
 Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala
 265 270 275
 gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag 979
 Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys
 280 285 290
 gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat
 1027
 Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp
 295 300 305
 gtc tcc ctg tgacttggtc caattacatt cac
 1059
 Val Ser Leu
 310

<210> 868
 <211> 312
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 868
 Met Val Gly Ser Ser Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr
 1 5 10 15
 Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe
 20 25 30
 Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn
 35 40 45
 Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala
 50 55 60
 Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn
 65 70 75 80
 Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu
 85 90 95
 Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu
 100 105 110
 Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu
 115 120 125
 Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr
 130 135 140

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
 145 150 155 160

Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
 165 170 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
 180 185 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
 195 200 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
 210 215 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
 225 230 235 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
 245 250 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
 260 265 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
 275 280 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
 290 295 300

Gln Ala Leu Asp Asp Val Ser Leu
 305 310

<210> 869

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> RXS03074

<400> 869

tttgtggggca atctggtttt ttcgtaattg tgtgggatga atctcttaaa aattcacatt 60

tagcaggaca agcatactgt tttagtttcta tgctgtgggc atg act caa agt gct 115
 Met Thr Gln Ser Ala
 1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259

Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165
 cag taatttggtt tgacgacgca gta 621
 Gln

<210> 870

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 870

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr

100	105	110	
Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr			
115	120	125	
Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe			
130	135	140	
Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr			
145	150	155	160
Glu Ala Pro Ile Lys Gln			
165			
<210> 871			
<211> 621			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(598)			
<223> FRXA02906			
<400> 871			
tttgtgggca atctggtttt ttcgtaattg tgtgggatga atctcttaaa aattcacatt	60		
tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct	115		
	Met Thr Gln Ser Ala		
	1 5		
cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac	163		
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn			
	10 15 20		
gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa	211		
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu			
	25 30 35		
ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc	259		
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu			
	40 45 50		
ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc	307		
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile			
	55 60 65		
gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca	355		
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala			
	70 75 80 85		
gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca	403		
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala			
	90 95 100		
att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc	451		
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala			
	105 110 115		
ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga	499		

Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165
 cag taatttgttt tgacgacgca gta 621
 Gln

<210> 872

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 872

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140
 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160
 Glu Ala Pro Ile Lys Gln
 165

<210> 873

<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
 145 150 155 160

Ala S r Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
 165 170 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
 180 185 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
 195 200 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
 210 215 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
 225 230 235 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
 245 250 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
 260 265 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
 275 280 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
 290 295 300

Gln Ala Leu Asp Asp Val Ser Leu
 305 310

<210> 869

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> RXS03074

<400> 869

tttgtgggca atctggtttt ttcgtaattg tgtgggatga atctcttaaa aattcacatt 60

tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
 Met Thr Gln Ser Ala
 1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259

Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165
 cag taatttggtt tgacgacgca gta 621
 Gln

<210> 870

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 870

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr

100 105 110
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140
 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160
 Glu Ala Pro Ile Lys Gln
 165

<210> 871
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(598)
 <223> FRXA02906

<400> 871
 tttgtgggca atctggtttt ttcgtaattg tgtgggatga atctcttaaa aattcacatt 60
 tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
 Met Thr Gln Ser Ala
 1 5
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35
 ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499

Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165
 cag taatttgttt tgacgacgca gta 621
 Gln

<210> 872

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 872

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140
 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160
 Glu Ala Pro Ile Lys Gln
 165

<210> 873

<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1729)

<223> RXA02315

<400> 873

```

cgtttgga cgccttgctgc cagcaaagat aggcgtgatt ggtgggtttga gcgcgtgcgt 60

gaatcgtatc cgtacctgga gacgatctag actgttgctgc atg tcc agc acg cca 115
Met Ser Ser Thr Pro
1 5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
10 15 20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tgc ctt 211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu
25 30 35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu
40 45 50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307
Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg
55 60 65

ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355
Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu
70 75 80 85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403
Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu
90 95 100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr
105 110 115

att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499
Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile
120 125 130

act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg 547
Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu Ser Leu Ala Gln Gly
135 140 145

gct tcc cag att ccg cgt cat ttc aat ctt gca ctt gat gtt cct ttg 595
Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala Leu Asp Val Pro Leu
150 155 160 165

gtt gct cct gaa ctg cca gag ctt cat ggt gag gca gtt gga gca tca 643
Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu Ala Val Gly Ala Ser
170 175 180

tgg acg cat cgc tgg atc aac cac ggt gag gtg acc gtg gac ctg ggg 691
Trp Thr His Arg Trp Ile Asn His Gly Glu Val Thr Val Asp Leu Gly
185 190 195

gag cac acc ctc gtg att gcc ggt gat gaa gca tgg gaa gtg gaa ggg 739

```

Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala Trp Glu Val Glu Gly	
200 205 210	
ctg gaa gat gtg ccc acc atc gct gaa cct act gca cca aag cct tat	787
Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr Ala Pro Lys Pro Tyr	
215 220 225	
aat ccg gtg cac cca ctg gct gct gaa atc ttg ctg aag gag cag gtc	835
Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu Leu Lys Glu Gln Val	
230 235 240 245	
tcc gcg gaa ggc tat gtg gta aac acc agg cct gat cat gtg atc gtg	883
Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro Asp His Val Ile Val	
250 255 260	
gtg gga cac ccc acg ctg cac cgc gga gtg ttg aag ttg atg tca gat	931
Val Gly His Pro Thr Leu His Arg Gly Val Leu Lys Leu Met Ser Asp	
265 270 275	
cct ggc att aaa tta act gtg ctt tca cgc acc gat atc atc act gat	979
Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr Asp Ile Ile Thr Asp	
280 285 290	
ccc ggc cgc cat gcc gat cag gtg ggc agc aca gtg aaa gtc acc ggc	
1027	
Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr Val Lys Val Thr Gly	
295 300 305	
acc cag gaa aag cag tgg cta aag atc tgt tcg gca gca tca gaa ctt	
1075	
Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser Ala Ala Ser Glu Leu	
310 315 320 325	
gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc	
1123	
Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn Gln Glu Phe Gly Phe	
330 335 340	
acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc	
1171	
Thr Gly Leu His Val Ala Ala Ala Val Ala Asp Thr Leu Gly Thr Gly	
345 350 355	
gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg	
1219	
Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu	
360 365 370	
gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc	
1267	
Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val	
375 380 385	
gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct	
1315	
Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala	
390 395 400 405	
gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc	
1363	
Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala	

410 415 420
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc
 1411
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile
 425 430 435
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac
 1459
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn
 440 445 450
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt
 1507
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly
 455 460 465
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc
 1555
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser
 470 475 480 485
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac
 1603
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp
 490 495 500
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc
 1651
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser
 505 510 515
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca
 1699
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala
 520 525 530
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt
 1749
 Gln Gln Gln Ala Leu Met Asp Thr Val His
 535 540
 gcg
 1752

<210> 874
 <211> 543
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 874
 Met Ser Ser Thr Pro Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser
 1 5 10 15
 Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
 20 25 30
 Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
 35 40 45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
 50 55 60
 Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
 65 70 75 80
 Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
 85 90 95
 Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
 100 105 110
 Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
 115 120 125
 Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
 130 135 140
 Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
 145 150 155 160
 Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
 165 170 175
 Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
 180 185 190
 Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
 195 200 205
 Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
 210 215 220
 Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
 225 230 235 240
 Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
 245 250 255
 Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
 260 265 270
 Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
 275 280 285
 Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
 290 295 300
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
 305 310 315 320
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
 325 330 335
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
 340 345 350
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
 355 360 365
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe

370	375	380
Ser Pro Arg Gly Val	Ala Gly Ile Asp Gly	Ser Val Ala Gln Ala Ile
385	390	395 400
Gly Thr Ser Leu Ala Val	Gln Ser Arg His Pro Asp	Glu Ile Arg Ala
405	410	415
Pro Arg Thr Val Ala Leu Leu Gly	Asp Leu Ser Phe Leu His Asp	Ile
420	425	430
Gly Gly Leu Leu Ile Gly Pro Asp	Glu Pro Arg Pro Glu Asn Leu Thr	
435	440	445
Ile Val Val Ser Asn Asp Asn Gly Gly Gly	Ile Phe Glu Leu Leu Glu	
450	455	460
Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe	Glu Arg Ala Phe Gly Thr	
465	470	475 480
Pro His Asp Ala Ser Ile Ala Asp Leu Cys	Ala Gly Tyr Gly Ile Glu	
485	490	495
His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp		
500	505	510
Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg		
515	520	525
Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His		
530	535	540

<210> 875

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1057)

<223> RXA02319

<400> 875

```

atgtgggtga gataaccgac cgtgatgtcg ccctagcaaa agtcacgac gccacgcca 60
agaccttggc catttcggca gaggccttaag gttaaagatt atg agc aac tac agc 115
                                     Met Ser Asn Tyr Ser
                                     1 5

acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
                10                15                20

gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
                25                30                35

gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn
                40                45                50

```

gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His 55 60 65	307
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly 70 75 80 85	355
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln 90 95 100	403
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg 105 110 115	451
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys 120 125 130	499
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg 135 140 145	547
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly 150 155 160 165	595
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg 170 175 180	643
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp 185 190 195	691
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn 200 205 210	739
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met 215 220 225	787
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu 230 235 240 245	835
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr 250 255 260	883
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu 265 270 275	931
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met 280 285 290	979

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa
 1027
 Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu
 295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct
 1077
 Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
 310 315

aaa
 1080

<210> 876
 <211> 319
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 876
 Met Ser Asn Tyr Ser Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala
 1 5 10 15
 Thr Val Pro Gly Phe Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His
 20 25 30
 Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
 35 40 45
 Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
 50 55 60
 Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
 65 70 75 80
 Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
 85 90 95
 Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
 100 105 110
 Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
 115 120 125
 Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
 130 135 140
 Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
 145 150 155 160
 Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
 165 170 175
 Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
 180 185 190
 Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
 195 200 205
 Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr
 210 215 220

Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp
 225 230 235 240
 His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn
 245 250 255
 Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu
 260 265 270
 Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr
 275 280 285
 Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe
 290 295 300
 Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
 305 310 315

<210> 877
 <211> 1017
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(994)
 <223> RXS00393

<400> 877
 tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tatttcaagc 60
 aattgcgcga tcgagtatgt gatgggggaaa gatagagggt atg tct cac acg gaa 115
 Met Ser His Thr Glu
 1 5
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50
 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
 55 60 65
 tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
 70 75 80 85
 cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
 90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
 105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
 120 125 130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
 135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
 150 155 160 165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
 170 175 180

gcc gca gtt ggc gtg ggg tgc atg tct gct ggc gtg aac ttg gcc aac 691
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
 185 190 195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
 200 205 210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
 215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
 230 235 240 245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
 250 255 260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc 931
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile
 265 270 275

ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg 979
 Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu
 280 285 290

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc
 1017
 Ala Leu Ala Phe Ser
 295

<210> 878

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 878

Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp

1	5	10	15
Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val	20	25	30
Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp	35	40	45
Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val	50	55	60
Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp	65	70	75
Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys	85	90	95
Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala	100	105	110
Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly	115	120	125
Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro	130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly	145	150	155
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser	165	170	175
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly	180	185	190
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr	195	200	205
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys	210	215	220
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu	225	230	235
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu	245	250	255
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp	260	265	270
Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala	275	280	285
Val Leu Thr Gly Leu Ala Leu Ala Phe Ser	290	295	

<210> 879

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (982)

<223> FRXA00393

<400> 879

```

tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tatttcaagc 60

aattgcgcga tcgagtatgt gatggggaaa gatagagggt atg tct cac acg gaa 115
                                         Met Ser His Thr Glu
                                         1      5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
                        10                        15                        20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
                        25                        30                        35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
                        40                        45                        50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
                        55                        60                        65

tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
70                        75                        80                        85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
                        90                        95                        100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
105                        110                        115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
120                        125                        130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
135                        140                        145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
150                        155                        160                        165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
170                        175                        180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
185                        190                        195

```

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
 200 205 210
 gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
 215 220 225
 att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
 230 235 240 245
 cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
 250 255 260
 ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
 265 270 275
 gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
 Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp
 280 285 290

cat tagcgttttag ctaaaacgct ttt
 1005
 His

<210> 880
 <211> 294
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 880
 Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
 1 5 10 15
 Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
 20 25 30
 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
 35 40 45
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60
 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro

[illegible]

```
<210> 881
<211> 843
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101) .. (820)  
<223> RXA00391
```

[illegible]

ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag 307
 Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln
 55 60 65

gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat 355
 Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp
 70 75 80 85

ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403
 Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu
 90 95 100

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
 105 110 115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
 120 125 130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg
 135 140 145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
 150 155 160 165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
 170 175 180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
 185 190 195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
 200 205 210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
 215 220 225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
 230 235 240

tgc 843

<210> 882

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 882

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile
 1 5 10 15

```
<210> 883
<211> 384
<212> DNA
<213> Corynebacterium glutamicum
```

<400> 883
gccaacgagg gttggtttac cacctctgat tcaggtgaac tccacgacgg gattctcacc 60
gtgactggtc gcgtggatac ccgtcattga ttccggtgga ttg aag ttg cac cca 115
Leu Lys Leu His Pro

	1	5	
gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg			163
Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala			
	10	15	20
tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc			211
Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala			
	25	30	35
gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac			259
Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp			
	40	45	50
gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct			307
Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser			
	55	60	65
ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag			355
Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys			
	70	75	80
ctg ttt tagtcttcat tcttgctggc tgc			384
Leu Phe			

<210> 884

<211> 87

<212> PRT

<213> Corynebacterium glutamicum

<400> 884

Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys			
1	5	10	15
Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly			
	20	25	30
Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val			
	35	40	45
Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu			
	50	55	60
Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg			
	65	70	75
Arg Ala Ile Ala Lys Leu Phe			
	85		

<210> 885

<211> 705

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(682)

<223> RXA00997

<400> 885

```

ccccatctgtg gcagatcgaa tgcacccacc gcggagaagt cgtcgcacga accacactgc 60
gcaccatggt gctgaacaag tagccctata ctcgggcacc atg act aca tgg aaa 115
                                     Met Thr Thr Trp Lys
                                     1 5
gag ctc aca gat aac aac cca gcg cac tca gaa aac tac gcg cag cgc 163
Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu Asn Tyr Ala Gln Arg
                                     10 15 20
tgg cga aac ctc gcc gca gca ggc aat gat att tac ggc gaa gcc cgc 211
Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile Tyr Gly Glu Ala Arg
                                     25 30 35
ctc att gat gcc atg gca ccc agg gga gcg aaa atc ttg gat gct ggc 259
Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys Ile Leu Asp Ala Gly
                                     40 45 50
tgc ggc cag gga cgc atc ggt ggc tac ctg tcc aag caa ggc cac gat 307
Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser Lys Gln Gly His Asp
                                     55 60 65
gtt cta ggc aca gac ctt gat ccc atc ctg att gat tac gcc aag cag 355
Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile Asp Tyr Ala Lys Gln
                                     70 75 80 85
gac ttt cca gaa gct cgc tgg gtg gtg gga gat ctc tct gtt gat cag 403
Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp Leu Ser Val Asp Gln
                                     90 95 100
atc tca gag act gat ttt gat ctc att gtc tcc gcc ggc aac gtc atg 451
Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser Ala Gly Asn Val Met
                                     105 110 115
ggc ttt ctc gct gag gat ggt cgc gaa cct gca cta gcc aac att cac 499
Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala Leu Ala Asn Ile His
                                     120 125 130
cgc gca ctg ggc gcc gat ggc cgc gct gtc atc ggt ttc ggc gca gga 547
Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile Gly Phe Gly Ala Gly
                                     135 140 145
cgt gga tgg gtc ttt gga gac ttc ctc gaa gtc gca gaa cgc gtg ggc 595
Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val Ala Glu Arg Val Gly
                                     150 155 160 165
ctc gag ttg gaa aat gct ttt gag tct tgg gat ctt aag cct ttt gtc 643
Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp Leu Lys Pro Phe Val
                                     170 175 180
caa ggc tct gag ttc tta gtg gcg gta ttt acc aag aag taacacctct 692
Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr Lys Lys
                                     185 190
atcttgcacc tga 705

```

<210> 886

<211> 194

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 886

```

Met Thr Thr Trp Lys Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu
  1          5          10          15

Asn Tyr Ala Gln Arg Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile
      20          25          30

Tyr Gly Glu Ala Arg Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys
      35          40          45

Ile Leu Asp Ala Gly Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser
      50          55          60

Lys Gln Gly His Asp Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile
      65          70          75          80

Asp Tyr Ala Lys Gln Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp
      85          90          95

Leu Ser Val Asp Gln Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser
      100          105          110

Ala Gly Asn Val Met Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala
      115          120          125

Leu Ala Asn Ile His Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile
      130          135          140

Gly Phe Gly Ala Gly Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val
      145          150          155          160

Ala Glu Arg Val Gly Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp
      165          170          175

Leu Lys Pro Phe Val Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr
      180          185          190

Lys Lys

```

<210> 887

<211> 861

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(838)

<223> RXA02189

<400> 887

```

aatggcaaaa atgggcacat acgatactga tgggaccaat gggaaaacct caagccacca 60

attgagccag ttctctcaag caaaccgata ctggtgggat gtg gac gcg gcc gac 115
              Val Asp Ala Ala Asp
              1          5

```

tat cac gaa cgc cac cct tct tat tta ggc acg gat tcc gct cac ggc	163
Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr Asp Ser Ala His Gly	
10 15 20	
gag ttc tac tgg tgc ccc gag atg ctg cat gaa aaa gat gta cgt ctt	211
Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu Lys Asp Val Arg Leu	
25 30 35	
ctt ggc act ccc gca gca ctc tcc ggc aag aaa att tta gag atc ggt	259
Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys Ile Leu Glu Ile Gly	
40 45 50	
tgc ggc tgc gca ccg tgt gct cgg tgg ctg gcc aat gat gtt ccg aat	307
Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala Asn Asp Val Pro Asn	
55 60 65	
gcc ttt gtc acc gct ttc gac att tct tca caa atg ctc aaa tac gca	355
Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln Met Leu Lys Tyr Ala	
70 75 80 85	
ggg cac gac cat aac gta cac ctc gta cag gcc gat gca atg tca ctc	403
Gly His Asp His Asn Val His Leu Val Gln Ala Asp Ala Met Ser Leu	
90 95 100	
ccc tac gcc gac agt tcc ttt gac gtg gtc ttt tcc gtt ttc ggc gcc	451
Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe Ser Val Phe Gly Ala	
105 110 115	
atc ccc ttt gtg gag gat tcc gcc gca ctc atg aag gaa atc gcg cgc	499
Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met Lys Glu Ile Ala Arg	
120 125 130	
gtc ctc aaa ccc ggc gga cgc ctc att ttc tcc atc acc cac ccg atg	547
Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser Ile Thr His Pro Met	
135 140 145	
cgc tgg att ttc ctc gac gat ccc ggc ccc gca ggc ctc acc gcg atc	595
Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala Gly Leu Thr Ala Ile	
150 155 160 165	
acc agc tac ttc gac cag cgc ggc tac gtc gaa gaa gac gag gaa acc	643
Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu Glu Asp Glu Glu Thr	
170 175 180	
ggg gct tta agc tat gcg gaa cag cac cgc acc atg ggc gcg cgg atc	691
Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr Met Gly Ala Arg Ile	
185 190 195	
aat gag ctt atc gac gcc tcc ctc cac tta gat cac ctc atc gaa cca	739
Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp His Leu Ile Glu Pro	
200 205 210	
gaa tgg cca gat gag ttg gaa gaa aac tgg ggc caa tgg tca cca ctt	787
Glu Trp Pro Asp Glu Leu Glu Asn Trp Gly Gln Trp Ser Pro Leu	
215 220 225	
cga gga aag ctc ttc ccc ggg aca gca atc ttc ctc gcc acg tac cgc	835
Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe Leu Ala Thr Tyr Arg	
230 235 240 245	
ccc taaaaaacca acggcgctca ttt	861

Pro

<210> 888

<211> 246

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 888

Val	Asp	Ala	Ala	Asp	Tyr	His	Glu	Arg	His	Pro	Ser	Tyr	Leu	Gly	Thr
1				5					10					15	
Asp	Ser	Ala	His	Gly	Glu	Phe	Tyr	Trp	Cys	Pro	Glu	Met	Leu	His	Glu
			20					25					30		
Lys	Asp	Val	Arg	Leu	Leu	Gly	Thr	Pro	Ala	Ala	Leu	Ser	Gly	Lys	Lys
		35					40					45			
Ile	Leu	Glu	Ile	Gly	Cys	Gly	Ser	Ala	Pro	Cys	Ala	Arg	Trp	Leu	Ala
	50					55					60				
Asn	Asp	Val	Pro	Asn	Ala	Phe	Val	Thr	Ala	Phe	Asp	Ile	Ser	Ser	Gln
65					70					75					80
Met	Leu	Lys	Tyr	Ala	Gly	His	Asp	His	Asn	Val	His	Leu	Val	Gln	Ala
				85					90					95	
Asp	Ala	Met	Ser	Leu	Pro	Tyr	Ala	Asp	Ser	Ser	Phe	Asp	Val	Val	Phe
			100					105					110		
Ser	Val	Phe	Gly	Ala	Ile	Pro	Phe	Val	Glu	Asp	Ser	Ala	Ala	Leu	Met
		115					120					125			
Lys	Glu	Ile	Ala	Arg	Val	Leu	Lys	Pro	Gly	Gly	Arg	Leu	Ile	Phe	Ser
	130					135					140				
Ile	Thr	His	Pro	Met	Arg	Trp	Ile	Phe	Leu	Asp	Asp	Pro	Gly	Pro	Ala
145					150					155					160
Gly	Leu	Thr	Ala	Ile	Thr	Ser	Tyr	Phe	Asp	Gln	Arg	Gly	Tyr	Val	Glu
				165					170					175	
Glu	Asp	Glu	Glu	Thr	Gly	Ala	Leu	Ser	Tyr	Ala	Glu	Gln	His	Arg	Thr
			180					185					190		
Met	Gly	Ala	Arg	Ile	Asn	Glu	Leu	Ile	Asp	Ala	Ser	Leu	His	Leu	Asp
		195					200					205			
His	Leu	Ile	Glu	Pro	Glu	Trp	Pro	Asp	Glu	Leu	Glu	Glu	Asn	Trp	Gly
	210					215					220				
Gln	Trp	Ser	Pro	Leu	Arg	Gly	Lys	Leu	Phe	Pro	Gly	Thr	Ala	Ile	Phe
225					230					235					240
Leu	Ala	Thr	Tyr	Arg	Pro										
				245											

<210> 889

<211> 813

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(790)

<223> RXA02311

<400> 889

```

cattttgggt atcgggttgggt tgtccatcgg tggagctaag ggcgctaagc atcgagcca 60
aataacctcc cactaaagct cctgggttag actcgaacgc gtg gct aaa gca gat 115
Val Ala Lys Ala Asp
1 5
tta gac aag gac ccc ttc gac gta gcg tca atg ttc gat gac gtc gga 163
Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met Phe Asp Asp Val Gly
10 15 20
aag aac tac gat ctc acc aat acc gtg ctt tct ttt ggt cag gac cgt 211
Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser Phe Gly Gln Asp Arg
25 30 35
gtg tgg cga aag cgc act agg cag cgc ctg gac ctc aag cca ggg gag 259
Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp Leu Lys Pro Gly Glu
40 45 50
aag gtg ctt gat cta gct gca gga aca gcc gtt tcc acc gtg gag ttg 307
Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val Ser Thr Val Glu Leu
55 60 65
gca aaa tcc ggc gcg ttt tgt gtg gcg tgt gat ttc tcc cag ggc atg 355
Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp Phe Ser Gln Gly Met
70 75 80 85
ctc gcc gca ggt aaa gac cgc gat gtg tcc aag gtt gtg ggc gat ggc 403
Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys Val Val Gly Asp Gly
90 95 100
atg cag ttg ccg ttt gca gac aac agc ttt gat gct gtg acc att tct 451
Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp Ala Val Thr Ile Ser
105 110 115
tat ggt ctg cgc aat att cac gat ttc cgc gct ggc ctg aaa gaa atg 499
Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala Gly Leu Lys Glu Met
120 125 130
gcc cgc gtg act aaa cct ggt gga cgc ctc acc gtg gcg gag ttc tcc 547
Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr Val Ala Glu Phe Ser
135 140 145
acc ccc gtg atc cct gtg ttc ggc acc gtg tac aag gag tac ctc atg 595
Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr Lys Glu Tyr Leu Met
150 155 160 165
cgc ctg ctg ccc cag gcg gcg cgc gca gta tcg tcc aac ccg gag gcc 643
Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser Ser Asn Pro Glu Ala
170 175 180
tac att tac ctg gct gat tcc atc cgc gca tgg cct agc cag gcg gaa 691
Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp Pro Ser Gln Ala Glu

```

185	190	195	
cta gca cgg gag atc aac cag aat ggt tgg tca gat tgc ggt tgg cag			739
Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser Asp Cys Gly Trp Gln			
200	205	210	
aac ctg acc ttc ggc atc gtc gcg ctg cac tcg gcg att aaa cca gag			787
Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser Ala Ile Lys Pro Glu			
215	220	225	
aac tagtcgagtc ccacagaggg gag			813
Asn			
230			

<210> 890

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 890

Val	Ala	Lys	Ala	Asp	Leu	Asp	Lys	Asp	Pro	Phe	Asp	Val	Ala	Ser	Met
1				5					10					15	

Phe	Asp	Asp	Val	Gly	Lys	Asn	Tyr	Asp	Leu	Thr	Asn	Thr	Val	Leu	Ser
			20					25					30		

Phe	Gly	Gln	Asp	Arg	Val	Trp	Arg	Lys	Arg	Thr	Arg	Gln	Arg	Leu	Asp
		35					40					45			

Leu	Lys	Pro	Gly	Glu	Lys	Val	Leu	Asp	Leu	Ala	Ala	Gly	Thr	Ala	Val
50						55					60				

Ser	Thr	Val	Glu	Leu	Ala	Lys	Ser	Gly	Ala	Phe	Cys	Val	Ala	Cys	Asp
65					70					75					80

Phe	Ser	Gln	Gly	Met	Leu	Ala	Ala	Gly	Lys	Asp	Arg	Asp	Val	Ser	Lys
				85					90					95	

Val	Val	Gly	Asp	Gly	Met	Gln	Leu	Pro	Phe	Ala	Asp	Asn	Ser	Phe	Asp
		100						105					110		

Ala	Val	Thr	Ile	Ser	Tyr	Gly	Leu	Arg	Asn	Ile	His	Asp	Phe	Arg	Ala
		115					120					125			

Gly	Leu	Lys	Glu	Met	Ala	Arg	Val	Thr	Lys	Pro	Gly	Gly	Arg	Leu	Thr
130						135					140				

Val	Ala	Glu	Phe	Ser	Thr	Pro	Val	Ile	Pro	Val	Phe	Gly	Thr	Val	Tyr
145					150				155						160

Lys	Glu	Tyr	Leu	Met	Arg	Leu	Leu	Pro	Gln	Ala	Ala	Arg	Ala	Val	Ser
				165				170						175	

Ser	Asn	Pro	Glu	Ala	Tyr	Ile	Tyr	Leu	Ala	Asp	Ser	Ile	Arg	Ala	Trp
		180						185					190		

Pro	Ser	Gln	Ala	Glu	Leu	Ala	Arg	Glu	Ile	Asn	Gln	Asn	Gly	Trp	Ser
		195					200					205			

Asp	Cys	Gly	Trp	Gln	Asn	Leu	Thr	Phe	Gly	Ile	Val	Ala	Leu	His	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

210	215	220	
Ala Ile Lys Pro Glu Asn			
225	230		
<210> 891			
<211> 876			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(853)			
<223> RXN02912			
<400> 891			
catcgggtgtc gggttcactga tgggtggccaa gaaggttgga taacaggggtt aatcttgggt 60			
gatattgaaa tgacgtattc ctgattgggc tgaaaaatct gtg aca tca cct gaa 115			
Val Thr Ser Pro Glu			
1 5			
tta caa aac atc ctt aac aat tat tgg agc ggc agg gca gag gct tac 163			
Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly Arg Ala Glu Ala Tyr			
10 15 20			
cac ctc aac caa acc caa agc gag cgt gca caa ttt gaa cgc ccc atc 211			
His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln Phe Glu Arg Pro Ile			
25 30 35			
tgg gaa aag gtg tgg tcg aag gct ttg cct atc gtg tcg gaa gaa gcg 259			
Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile Val Ser Glu Glu Ala			
40 45 50			
gta aag gtt ctc gat ctt ggc tgt ggc gct ggt tat gtc acc cac ctt 307			
Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly Tyr Val Thr His Leu			
55 60 65			
cta agc gat tgc gga tac gaa aca atc ggc gtt gat ggt tct gag gaa 355			
Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val Asp Gly Ser Glu Glu			
70 75 80 85			
atg atc aat caa gct acg cag gag aat ggt ctt cgc agg tcg acg ggt 403			
Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu Arg Arg Ser Thr Gly			
90 95 100			
cgg gcg act gcc att ttt cag gtc ggg gat gcg cat gat ccc gag ttc 451			
Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala His Asp Pro Glu Phe			
105 110 115			
cgg gaa ggc tct ttt gat gcg ata acc agc cgg tat gtg ttg tgg act 499			
Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg Tyr Val Leu Trp Thr			
120 125 130			
ctg ctg gat ccc cag gca gcg att aat cgt tgg gtg tct ttg cta aaa 547			
Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp Val Ser Leu Leu Lys			
135 140 145			
cct ggt ggg gtt att gcg tgc gta gat gcg gct tgg tat ccg aag ggc 595			
Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala Trp Tyr Pro Lys Gly			